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GenCore version 5.1.6
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December 29, 2005, 22:08:41; Search time 6729 Seconds (without alignments) 12786.661 Million cell updates/sec OM nucleic - nucleic search, using sw model Run on:

US-09-696-686-47 1839 Title: Perfect score:

Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

82156650 41078325 segs, 23393541228 residues Total number of hits satisfying chosen parameters:

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

EST:* Database :

gb_gss1:* gb_gss2:* 99 est1: 99 est2: 99 est4: 99 est4: 99 est6: 90 est6: 90 est6: gb_gss3:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

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AKO49358.1 GI:26340087
AKBYWORDS ".HTC; CAP trapper.
SOURCE Mis musculus (house mouse)
OKGANISM Mis musculus Bequence RESULT 1 AK049358 LOCUS DEFINITION REFERENCE AUTHORS TITLE JOURNAL PUBMED REFERENCE ACCESSION PUBMED REFERENCE AUTHORS JOURNAL AUTHORS JOURNAL TITLE TITLE

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TITLE JOURNAL REFERENCE

REFERENCE AUTHORS

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Mature 420, 563-573 (2002)

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  PANTOM Consortium and the RIKEN Genome Exploration Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
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Copyright (c) 1993 - 2005 Compugen Ltd.
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ALIGNMENTS

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	ACTO-REGILATED PROTEIN) (RIKEN CDNA 1600025D17 GENE), full insert
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ACCESSTON	AK049358
VERSTON	AK049358 1 GT-26340087
KEYWORDS	10
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
	Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	1
AUTHORS	Carninci, P. and Hayashizaki, Y.
TITLE	High-efficiency full-length cDNA cloning
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)
PUBMED	10349636
REFERENCE	8
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
	<pre>Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.</pre>
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to
	prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)
PUBMED	11042159
REFERENCE	
AUTHORS	
	Konno.H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M.,
	Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
	Yamamoto.R., Matsumoto.H., Sakaquchi,S., Ikegami,T., Kashiwagi,K.,
	Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
	Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,
	Okazaki, Y., Muramateu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE	RIKEN integrated sequence analysis (RISA) system384-format
	sequencing pipeline with 384 multicapillary sequencer
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)
PUBMED	11076861
REFERENCE	
AUTHORS	The RIKEN Genome Exploration Research Group Phase 11 Team and the
77.77.0	FANION CONSTITUTION OF A full-length mouse cDNA collection
TOTTENAT	Nature 409, 685-690 (2001)
REFERENCE	100, 000 000 (100)

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TCCTGCCCCGAAGCTAGGCCCGAGTCCCGCCGGGGCTGAGGAGCCGACTGGGTGCGATT
                                     TCCTGCCCCGAAGCTAGGCCCGAGTCCCGCCGGGGCTGAGGAGACCGACTGGGTG
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/codon id="BAC33707.1"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Stangawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome-gsc.riken.jp/, Tel:81-45-503-9222, Rax:81-45-503-9216)
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                    Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 1832)
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      Exploration Research
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Please visit our web site for further details.
URL:http://gancome.gsc.riken.jp/
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Location/Qualifiers
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      FANTOM Consortium and the RIKEN Genome
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/db xref="taxon:10090"
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_gtage="0 day neonate"
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Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsunoto, H., Sakagurchi, S., Itsegami, T., Kashiwagi, K., Pujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J. Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer
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Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
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Please visit our web site for further details.
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/strain="C57BL/6J"
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6 (bases 1 to 1787)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AK086940
Mus musculus 0 day neonate lunc classes AFR-2004
Mus musculus 0 day neonate lunc classes full-length enriched
ibrary, clone:E030013D02 produce:1600025D17RIK PROTEIN (PUTATIVE
RETINOIC ACID-REGULATED PROTEIN) (RIKEN CDNA 1600025D17 GENE), full
         AGTGTCCCCTCATCGATCTTTTTTGCCTTTTGTCCCCCAATCCCAGGGGATAGAAGGCCAT 1648
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                    CCTGCCTCTTCCTTCCACCAAGCATTCTCTTCTGCTGGTCCTTGTCGGATGGTAAATTCG
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High-efficiency full-length cDNA cloning
The Enzymol. 303, 19-44 (1999)
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AK085617

Mus musculus 0 day neonate kidney cDNA, RIKEN full-length enriched library, clone:D630047M13 product:1600025D17RK PROTEIN (PUTATIVE RETINOIC ACID-REGULATED PROTEIN) (RIKEN CDNA 1600025D17 GENE), full insert sequence.

DN AK085617

AK085617

AK085617

HTC; CAP trapper.

Mus musculus (house mouse)

KINEN CDNA 1600025D17 GENE), full insert sequence.

Mus musculus (house mouse)

KINEN Mus musculus (house mouse)
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                                                                                                                  CCTCCCTTGGCTGTGCCCCTTTCCTTCCCTTGAACAACAACAAGAGGGTGGAAGGATCTGG
                            GACCTAACCCCCCTGGAAAGCCAATCTGCAGTTCCCGTGTCCACTCCTCCTCCTGAGGA
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ICKRLLDYSLHKERTGSNRFAKGMSETFETLHNLVHKGVKVVMDIPYELMNETSAEVA
DLKKQCDVLVEEFEEVIEDMYRNHQEEDLTEFLCANHVLKGKDTSCLAERWSGKKGDI
ASLGGKKSKKKRSGVKGSSSGSKQRKELGGLGEDANAEEEEGVQKASPLPHSPPDEL
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                                     /note="unnamed protein product; 1600025D17RIK PROTEIN (PUTATIVE RETINOIC ACID-REGULATED PROTEIN) (RIKEN CDNA 1600025D17 GENE) (SPTR|Q9DAU1, evidence: FASTY, 100%10.100%1ength, match=828)
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNs.

Le 60,770 full-length cDNs.

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Redchi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hashizume, W., Hayakida, K., Hayaku, T., Hashizume, W., Hayakida, S., Furuno, M., Hanagaki, T., Hanacka, T., Haraka, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Komno, H., Kouda, M., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Komno, H., Kouda, M., Katoh, H., Sakai, K., Ohno, M., Obsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Saito, H., Sakai, K., Sakai, K., Saitoh, H., Sakai, K., Sakai, K., Saitok, Y., Saito, M., Tagawa, A., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
                                                                                                     Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected CDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
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Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research Stroup, RIKEN , Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome-gsc.riken.jp/, Tel:81-45-503-9212,
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
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Please visit our web site for further details.
URL:http://genome.gec.riken.jp/
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
  Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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/db_xref="taxon:10090"
/dbom="n530047M13"
/tissue_type="kidney"
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EEDLTEFLCANHVLKGKDTSCLAERWSGKKGDIASLGGKKSKKKRSGVKGSSSGSSKQ
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                                                                                                                                                                                                                                                                                              /protein id="BAC27534.1"
/db xref="G1:26327581"
/translation="PAPKLGPSPAGAEETDWVRLPSKCEVCKYVAVELKSAFEETGKT
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Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL:http://fenome.gsc.riken.jp/.

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Location/Qualifiers
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                                                                                                                /mol_type="mRNA"
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/clone="6230400B22"
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clone_lib="RIKEN full-length
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100.0%; Pred
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/codon_start=2
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                                                                                      GAACTGGGGGGCCTGGGGGAGGATGCCAACGCCGAGGAGGAGGAGGGTGTGCAGAAGGCA
                                                                                                                                   TCGCCCCTCCCACACACCCCCCCTGATGAGCTGTGAGCCCCAGCTTAGTGTCCTTGAATCA
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/protein id="BAB24103.1"
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ICKRLLDYSLHKERTGSNRFAKGMSFTFETLINLHVKGVKVNDIPYELWNETSARVA
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
dev stage="adult"
               Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, WRL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Pax:81-45-503-9216)
                                                                                                                                                                        Please visit our web site (http://genome.gsc.riken.jp/) for further
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Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
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/mol_type="mRNA"
/strain="C5TBL/6J"
/db_xref="FANTOM DB:1600025D17"
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100.0%; Pred. No. 0;
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                                                                                                                                                                                                                                                                             AK005532 Ilnear HTC 03-AFR-2004 Mus musculus adult female placenta cDNA, RIKEN full-length enriched library, clone:1600025917 product:1600025917RIK PROTEIN (PUTATIVE RETINOIC ACID-REGULATED PROTEIN) (RIKEN CDNA 1600025917 GENE), full
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Yoneda, Y., Ishikawa, T., Ozawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format genome Res. 10 (11), 1757-1771 (2000)
     CTTCTGTTGTGGTGACTCCCACGCCCCACACACACCATAAAATTATTTCGATGCTGT 1809
                            Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
6 60,770 tull-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 1553)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Oy 1389 CGCCAGAGACTGCAGAGAGAGACTGTGACTAACC	RESULT 6 AK082340 LOCUS DEFINITION MUS MUSCULUS 0 day neonate cerebellum enriched library, clone:(230039609 px (PUTATIVE RETINOIC ACID-REGULATED PRC GENE), full insert sequence. ACCESSION AK082340. IG:26349662 KEYWORDS HTC; CAP trapper. SOURCE ORGANISM Mus musculus (house mouse) ORGANISM Mus musculus (house mouse) Mus musculus (house mouse) SOURCE Bukaryota; Metazoa; Chordata; Craniat Mamania; Eutheria; Euarchontoglires; Sciurognathi; Mutidae; Musinae; Musin	REFERENCE AUTHORS Carninci, P. and Hayashizaki, Y. TUTLE High-efficiency full-length cDNA clor JOURNAL Meth. Enzymol. 303, 19-44 (1999) 10349636 REFERENCE AUTHORS Itoh, M., Konno, H., Okazaki, Y., Murama TITLE Normalization and subtraction of capprepare full-length cDNA libraries for JOURNAL Genome Res. 10 (10), 1617-1630 (2000)	AUTHORS Sibata,K., Itoh,M., Aizawa,K., Nagac Konno,H., Akiyama,J., Nishi,K., Kitsu Sumi,N., Ishii,Y., Nakamura,S., Hazar Yamamoto,R., Matsumoto,H., Sakaguchi, Fujiwake,S., Inoue,K., Togawa,Y., Iza Yoneda,Y., Ishikawa,T., Ozawa,K., Tan Okazaki,Y., Muramatsu,M., Inoue,Y., R TITLE RIKEN integrated sequence analysis (R sequencing pipeline with 384 multical PUBMED 11076861	TITLE TOURNAL TITLE TOURNAL TITLE TOURNAL TITLE Nature 409, 685-690 (2001) REFERRNCE AUTHORS THE FANTOM CONSORTIUM and the RIKEN G Group Phase I & II Team. TITLE Analysis of the mouse transcriptome of 60,770 full-length cDNAs JOURNAL REFERENCE Adachi,J., Aizawa, K., Akimura,T., Ara AUTHORS Adachi,J., Aizawa, K., Akimura,T., Hayashida, K., Hayatsu,N., Hiramoto, K. Hori,F., Imotani,K., 18hii,Y., Itoh,M. Katoh,H., Kawai,J., Kojima,Y., Kondo, Koya,S., Kurihara,C., Matsuyama,T., M. Nakamara,M., Nishi,K., Nomura,K., Num Okazaki,Y., Satoh,H., Sakasi,D., Shibata,K., Shina
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Co, K., Hiraoka, T., Hirozane, T.,
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ndo, S., Konno, H., Kouda, M.,
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KKRSGVKGSSSGSSKQRKELGGLGEDANAEEEEGVQKASPLPHSPPDEL"
Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

Muramatsu,M. and Hayashizaki,Y.

Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIRKN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, MUR.http://genome-gsc.riken.jp/, Tel:81-45-503-9222,
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Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
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/note="unnamed protein product; 1600025D17RIK PROTEIN
(PUTATIVE RETINOIC ACID-REGULATED PROTEIN) (RIKEN CDNA
1600025D17 GENE) (SPTR Q9DAU1, evidence: PASTY, 100%ID,
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Division of Experimental Animal Research in Riken contributed prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
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Best Local Similarity 99.4%; Pred. No. 0;
Matches 1368; Conservative 0; Mismatches
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNas

Loud 1376,

Nature 420, 563-573 (2002)

E & (bases I to 1376)

Radachi, J., Alzawa, K., Akimura, T., Hara, A., Hashizume, W.,

Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,

Hayashida, K., Hayatsu, M., Hirankor, T., Hiraoka, T., Hiraoka, T.,

Ratoh, H., Kawai, J., Kojima, Y., Itoh, M., Kagawa, I., Kasukawa, T.,

Katoh, H., Kawai, J., Kojima, Y., Itoh, M., Kagawa, I., Kasukawa, T.,

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Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,

Sano, H., Sasaki, T., Tomaru, A., Toya, T., Yabunishi, A.,

Muramateu, M., and Hayashizaki, Y., Toya, T., Yabunishi, A.,

Muramateu, M., and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Pujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Warchiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-1384-format Genome Res. 10 (11), 1757-1771 (2000)
                          AK082749

MUS MUSCULUS ES CELLS CDNA, RIKEN FULL-LENGTH ENTIT COT-APR-2004

MUSCULUS ES CELLS CDNA, RIKEN FULL-LENGTH ENTITCHEd LIbrary,

CLORE: C330002N05 product: 1600025D17RIK PROTEIN (PUTATIVE RETINOIC

ACID-REGULATED PROTEIN) (RIKEN CDNA 1600025D17 GENE), full insert
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Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
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Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The RIKEN Genome Exploration Research Group Phase II Team and
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Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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HTC; CAP trapper.
Mus musculus (house mouse)
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Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

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S Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Ruuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Sakai, C., Sakai, C., Sakai, C., Sakai, T., Sono, H., Sasaki, D., Shibata, K., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Tagawa, A., Yasunishi, P., Yasunishi, P., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Shibata, M., and Hayashizaki, Y., Toya, T., Yasunishi, A., Yoshida, K., Yoshida, K., Yoshida, K., Allanaki, Y., Toya, T., Yasunishi, Y., Toya, T., Yasunishi, Y., Toya, T., Yasunishi, A., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yasunishi, Y., Toya, Y., Toya, Y., Toya, Yoshida, K., Yoshida, K., Yasunishi, Y., Toya, Y., Yasunishi, Yas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Please visit our web site (http://genome.gsc.riken.jp/) for further
                                                                                                                                                                                                                                                                                                                                                                                        Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384-format genencing pipeline with 384 multicapillary sequencer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The RIKEN Genome Exploration Research Group Phase II Team and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoha (Ranagawa 230-0045, Japan (E-mail:genome-resegsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The FANTOM Consortium and the RIKEN Genome Exploration Research
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Nature 409, 685-690 (2001)
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/db_xref="taxon:10090"
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/mol_type="mRNA"
/strain="C57BL/6J"
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Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muridae, Murinae, Mus.
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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REFERENCE AUTHORS TITLE JOURNAL

ACCESSION VERSION KEYWORDS

AK010702 RESULT 8

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1679 CCCGGGGTTCGTTTCGGGTAATCACTCGCTCTCAGCCTTCTAACACTGCAGCCCCT 1738
1475 CCCGGGGTTGGTTTGGGGTAATCACTGGCTCTCAGCCTTCTAACACTGCAGCCCT 1534
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HESC2 41 D10.g1 A035 NIH MGC 258 Homo sapiens cDNA clone
TMADE:7470381 57, mRNA sequence.
CX166520
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Email: cgapbs-femail.nih.gov
Tissue Procurement: Bresaden, Inc.
cDNA Library Preparation: Express Genomics, Inc.
cDNA Library Preparation: Express Genomics and Bioinformatics,
University of Georgia
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLMM15772 row: g_column: 19
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Hominidae, Homo.

I (basea I to 766)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                   GCCAGAGCCACGCCAGAGACTGCAGAGAGGGCACCTGACCTGACCCCCTGGAAAGCCAA
                                                                                                                                                                                                                                           1295 CTCCCAGGGCTACCAGAGTAAACACCTTTTGGCCTTTCGGTTTGGTTCCTGGGTCCTCAT
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 1055 AGCAGCCAGGCCTGCCTCTTCCACCAAGCATTCTCTTCTGCTGGTCCTTGTCGGAT
                                                                                                                                                           TCTGCAGTTCCCGTGTCCACCCACCCTCCTGAGGACGCCTCATGCTCTGCCCAGCCCTT
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Seg primer: JENREV (CAGGAAACAGCTATGACC)
High quality sequence stop: 766.
Location/Qualifiers
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1 (bases 1 to 766)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                              661 GAAGGGGGACATAGCCTCCCTGGGAGGAAGAATCCAAGAAGAAGCAGCGCAGCGGAGTCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MCC clone distribution information can l
found through the I.M.A.G.B. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10978 row
High quality sequence stop: 761.
Location/Qualifiers
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/mol_type="mRNA"
/strain="NMRI"
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                                                                                                                                                                                                           /clone libe MILL MATE FARE 1: NOLI; Site 2: ECORV; NOTE="Weetor: pExpress-1; Site 1: NOLI; Site 2: ECORV; RNA obtained from human embryonic stem cells isolated from the inner cell mass of blastocyse stage embryos and differentiated to an early endodermal cell type. Cell line id and NIH Registry designation is BGO1. Positive for GATA4, MixLi, MaxLi, HNF4Alpha expression; negative for AFP expression. Passage number 40. cDNA primed using oligo-dT primer: S'-pGACTAGTTCTAGATGCGGAGGGGCGCCC(T)25-3' and cloned into the EcoRV/NotI sites of pExpress-1. This primary library is non-normalized (normalized primary library is non-normalized (normalized primary library is non-normalized (normalized by Express Genomics (Frederick, MD). Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA. Note: this is a Mammalian Gene Collection library."
                                                 /tissue type="human embryonic stem cells differentiated to an early endodermal cell type"
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                                                                                                                                                                                    /lab_host="DH10B-T1 phage-resistant E. coli"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                      cell_type="human embryonic stem cells" cell_line="BG01"
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100.0%; Pred. No. 7.7e-179;
ive 0; Mismatches 0;
clone="IMAGE:7470381"
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/mol_type="mRNA"
/db xref="taxon:10090"
/db xref="taxon:10090"
/clone="LMAGE:646664"
/clone="Lype="return"
/lab_host="DHLOB (phage-resistant)"
/clone_lib="NIH_MGC_94"
/clone="Corgan: eye, Vector: pCMV-SPORT6; Site_1: NotI;
/note="Corgan: eye, Vector: pCMV-SPORT6; Site_1: NotI;
/site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average inser size 3:3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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llarity 99.2%; Pred. No. 3.4e-175;
Conservative 0; Mismatches 6;
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5', mRNA sequence.
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NIH-MGC http://mgc.nci.nih.gov/.
NIH-MGC http://mgc.nci.nih.gov/.
Nutional Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLML)
DNA Sequencing by: Agencourt Bioceience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://inage.llnl.gov
Plate: LLAM13996 row: i column: 17
High quality sequence stop: 632.
High quality sequence stop: 632.
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Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Murcidea; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Sopher-wail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Prayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://inage.lln.gov
Plate: LLAMI1097 row: f column: 23
High quality sequence stop: 784.
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/clone="IMAGE:5035030"
/tissue type="spontaneous tumor, metastatic to mammary.
Stem cell origin."
/lab host="Drigin."
/clone lib="NCI_CGAP_Lu29"
/note="Origan: lung; Vector: pCMV-SPORT6; Site_1: Sal1;
Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
         'n
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
602890091F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:5035030
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Pred. No. 2.5e-173;
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    .793
    organism="Mus musculus"

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/strain="Czech II"
                                                                                                                                                       Mus musculus (house mouse)
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//mol type="mana"
//db xref="taxon:10090"
//dlome="Imana:1014242"
//dlome="taxon:10090"
//dlome="taxon:100
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NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. David Rowe
CDNA Library Preparation: Invitrogen Corp
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM0051 row: k column: 07
High quality sequence stop: 609.
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IMAGE:30142422 5', mRNA sequence.
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NIH-MGC http://mgc.ncl.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Gapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at:
http://image.llnl.gov
http://image.llnl.gov
High quality sequence stop: 608.
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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/mol_type="mRNA"
/strain="FVB/N-3"
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/clone="IMAGE:6528637"
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/clone lib="Organ of Corti"
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Sine_1: EcoRi; Site_2: Xho1; The organ of Corti (OC) was
Site_1: EcoRi; Site_2: Xho1; The organ of Corti (OC) was
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AGENCOURT_15614073 Organ of Corti Mus musculus cDNA clone IMAGE:30519414 5', mRNA sequence.
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                                                                                                   CCCAATCCCAGGGGCTGGAAGGCCATCACCATCATTGGAGGCTTAACCTGTCAGTTACTA 600
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Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Genomics
National Cancer Genomics
Figure From Cancer Thatitute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Bechara Rachar Achar, Celine Pompeia, NIDCD.
CDNA Library Preparation: Bechara Rachar, Celine Pompeia, NIDCD
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LANL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://imago.llnl.gov
Plate: NDAM590 row: o column: 07
High quality Sequence Stop: 579.
High quality Sequence Stop: 579.
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NIH-WGC http://mgc.nci.nih.gov/.
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AUTHORS
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in GenBank and have know function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified. Library created in the laboratory of M. Brownstein (NIMH, NIH) complete library decription can be found at ."
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Pred. No. 8.8e-171;
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Job time : 6737 secs
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ilarity 97.9%;
Conservative 0
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Homo sapi Gallus ga

Homo sapi Xenopus I Danio rer Xenopus I Homo sapi Sequence Mus muscu Sequence Sequen

AX198855 Sc AX209935 Sc CR524291 Gc CR524291 Gc BC022033 Hc BC083297 Dc BC083297 Dc BC083297 Dc BC08425 Hc AXC96425 Hc AXC96425 Hc AXC96425 Hc AXC96425 Hc AXC96425 Hc BC0864426 Dc BC0864426 Dc BC0866425 Dc BC086665 Dc BC086

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ALIGNMENTS	BC013549 1882 bp mRNA linear ROD 28-SEP-2004 N Mus musculus trinucleotide repeat containing 5, mRNA (cDNA clone MGC:19340 IMAGE:4222133), complete cds. BC013549 BC013549. GC13549.1 GI:15488835 MGC. MMS musculus (house mouse)	E	Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length	
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/product="trinucleotide repeat containing 5"
/product="trinucleotide repeat containing 5"
/protein_id="AAH13549.1"
/db_xref="di-18488836"
/db_xref="di-1912929"
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/db_xref="wdi-191202"
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/db_xref="wdi-191202"
/db_xref="wdi-1912
                                                                                                                                                                                                                                                                                                                                                       be found
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 31982623.

I. ols82
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                                           WIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 943
Meb site: Dickson, Mark) mcd@paxil.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
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/clone="MGC:19340 IMAGB:4222133"
/tissue_type="Kidney, normal. 5 "
/clone_lib="NCI_CGAP_Kid14"
/lab_host="DH10B"
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Pred. No. 0;
0; Mismatches
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/mol_type="mRNA"
/strain="FVB/N"
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'note="synonyms: CAG4A,
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/mol type="mcNA"
/db xref="taxon:10090"
/cell line="Pl9; derived from matings between C3H/He females and male animals carrying an X chromosome derived from a feral mouse (McBurney & Rogers, Dev. Biol., 89, 503)"
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    and Rogers, M.B.
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                                CCGTGTCCACCCACTCCTCAGGACGCCTCATGCTCTGCCCAGCCCTTCTCCCAGGGC
                                                                            CGGTGTCCACCCACCCTCCTGAGGACGCCTCATGCTCTGCCCAGGCCTTCTCCCAGGGC
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/product="putative retinoic acid-regulated protein"
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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Glozak, M.A., Li, Y., Reuille, R., Kim, K.H., Vo, M.N.
Trapping and characterization of novel retinoid re
Mol. Endocrinol. 17 (1), 27-41 (2003)
12511604
2 (bases 1 to 1909)
Glozak, M.A., Li, Y., Reuille, R. and Rogers, M.B.
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Glozak,M.A., Li,x.,
Glozak,M.A., Li,x.,
Direct Submission
Submitted (15-MAR-2001) Biology, Universe.
B. Fowler Avenue, Tampa, FL 33620, USA
Location/Qualifiers
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Okazaki,N., Kikuno,R.F., Ohara,R., Inamoto,S., Kitamura,H.,
Nagase,T., Ohara,O. and Koga,H.
Ragase,T., Ohara,O. and Koga,H.
Prediction of the Coding Sequences of Mouse Homologues of KIAA
Gene. The Complete Nucleotide Sequences of Mouse KIAA-homologous
CDNAS Identified by Screening of Terminal sequences of cDNA Clones
Randomly Sampled from Size-Fractionated Libraries.

L. Published Only in Database (2005)
2 Chases 1 to 1655)
3 Okazaki,N., F.Kikuno,R., Nagase,T., Ohara,O. and Koga,H.
Direct Submission
L. Submitted (22-FEB-2005) Hisashi Koga, Kazusa DNA Research
Institute, Laboratory for Genome Informatics, 2-6-7
Kazusa-kamatari, Kisarazu, Chiba, 292-0818, Japan
(E-mail:mouse@kazusa.or.jp, Tel:81-438-52-3918)
1 Location/Qualifiers
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VHKGVKVVMDIPYELMNETSAEVADLKKQCDVLVEEFEEVIEDWYRNHQEEDLTEFLC
ANHVLKGKDTSCLAERWSGKKGDIASLGGKKSKKKRSGVKGSSSGSSKQRKELGGLGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="CDS is predicted by in silico analysis. Start codon
is not identified."
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Pred. No. 0;
0; Mismatches 16; Indels 23;
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
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/note="vector:modified pBC 6
                                             Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <1. .1655
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01-MAR-2005

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linear

MAS musculus mRNA for mFLJ00338 protein. AK220209 AK220209.1 GI:60359829 FLI_CDNA.

DEFINITION ACCESSION VERSION KEYWORDS

RESULT 3 AK220209

LOCUS

1594 CCTTTGTCCCCAATCCCAGGGGTGGAAGGCCATCACC 1436 CCTTTGTCCCCCAAGGGGTGGAAGGCCATCACC 1654 CAGTTACTAGGAGGTGCTGGGAGGGCTGGGTTGGTTT 1496 CAGTTACTAGGAGGTGCTGGGAGGGCCCGGGGTTGGTTT 1714 TCAGCCTTCTAACACTGCAGCCCCTTAATACAGTTGCTT 1719TTTCTAACACTGCAGCCCCTTAATACAGTTCCTT 1553TTTCTAACACTGCAGCCCCTTAATA-TTTCGATC 1769 -CACGCCCCACACACACACACATAATA-TTTCGATC 1608 GCCCCACCCACACACACACATAATTTTCGTTC	SULT 4 008898 CUS ECO08898 ENITION Homo sapiens trinuclectide repeat contain MGC.1220 IMAGE:2959532), complete cds. CESSION BC008898 CESSION BC008898.2 GI:33870484 FRYORN MGC. Homo sapiens (human) ORGANISM Homo sapiens (human) ELKATYOTA; Metazoa; Chordata; Craniata; Nemmania; Eutheria; Euarchontoglires; Pri Hominidae; Homo. FERENCE I (bases 1 to 1413) AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L., & Altschul, S.F., Zeeberg, B., Buetow, K.H., & Altschul, S.F., Zeeberg, B., Buetow, K.H., & Hopkins, R.P., Oordan, H., Moore, T., Max, S., Stapleton, M., Soares, M.B., Bonaldo, M.F., Stapleton, M.F.	Scheetz, T.E., Brownstein, M.J., Usdin, T.B. Carninci, P., Prange, C., Raha, S.S., Loquel Abraman, R.D., Mullahy, S.J., Bosak, S.A., McKernan, K.D., Malek, J.A., Gunaratne, P.H. Worley, K.C., Hale, S., Garcia, A.M., Gay, L. Villalon, D.K., Muzny, D.M., Sodergren, E.J. Fahey, J., Helton, B., Ketteman, M., Madan, J. Sanchez, A., Whiting, M., Madan, A., Young, P. Bouffaad, G., Blakesley, R.W., Touchman, Dickson, M.C., Rodriguez, A.C., Grimwood, J. Butterfield, Y.S., Krzywinski, M.I., Skals) Schnerch, A., Schein, J.E., Jones, S.J. and TITLE Generation and initial analysis of more thuman and mouse cDNA sequences JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16	
8 8 8 8 8 8 8	RESULT 4 BC008898 LOCUS DEFINITION ACCESSION VERYONS KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS	TITLE	PUBMED REFERENCE AUTHORS TITLE JOURNAL COMMENT
		1054 GGGTGCTGGGAGCCCCCAAAGGAAGGAGGAGGAGCAGAGGCAGTCTTTT 1113 896 GGGTGCTGGGAGCCCCCAAAGGAAGGAAGGAGGAGCAGCTCTTTT 1113 896 GGGTGCTGGGAGCCCCCTAAAGGAAGGAAGGAGAGCAGCTCCTTT 955 1114 CTACACAGTCCCCCTCAGAGGTCCCCGGGATCCCCAGGTGAGATCCAGG 1173	1294 TCTCTTCTGCTGGTCCTTGTCGGATGGTAAATTCGAGAACTTCCAGGACAAACTCGGGTG 1353
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se, L.H., Derge, J.G.,
.., Shenmen, C.M., Schuler, G.D.,
.x, S.Lu, Wang, J., Hath, F.,
.x, S.L., Wang, J., Hath, F.,
.A., Rubin, G.M., Hong, L.,
.R., Casavant, T.L.,
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.R., McEwan, P.J.,
.N., McEwan, P.J.,
.N., Halyk, S.W.,
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.Y.L.J., Hulyk, S.W.,
E.J., Hulyk, S.W.,
E.J., Lu, X., Gibbs, R.A.,
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.ng, A.C., Shevchenko, Y.,
.anh, A., Green, E.D.,
.anh, J.W., Green, E.D.,
.anh, J.W., Smailus, D.E.,
.and Marra, M.A.
and Marra, M.A. TTTGGGGTAATCACTCACTGGCTC 1713 TTCTGTTGTGGTGACTCC---- 1768 ACCATCATTGGAGGCTTAACCTGT 1653 A linear PRI 29-JUN-2004 ining 5, mRNA (cDNA clone Vertebrata; Euteleostomi; rimates; Catarrhini; utes of Health, Mammalian Office, National Cancer Bethesda, MD 20892-2590, Mark Ketteman, Anuradha and Michelle Whiting .gov eplaced gi:14286203. ory Consortium (LLNL) ns Biology 16899-16903 (2002)

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AGCAGTGTGACGTGCTGGTGGAAGAGTTTGAAGAGTGATTGAGGACTGGTACAGGAACC
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIANL at: http://image.llnl.gov Series: IRAL Plate: 2 Row: m Column: 12
This clone was eelected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 5729791.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                    LPSKCEVCKYVAVELKSAFEETGKTKEVIGTGYGILDQKASGVKYTKSDLRLIEVTET
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EL"
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84.5%; Pred. No. 1.9e-158;
ive 0; Mismatches 139; Indels 6;
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                                                                                                                                                                                                                          1. 1413
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                                                                                                                                                                                                            /note="Vector: pOTB7"
                                                                                                                                                                                                                                                                                                  gene="TNRC5"
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Straubberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Rlausner, R.D., Collinns, F.S., Wagner, L., Shemmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

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Diatchenko, L., Marusina, K., Farmer, A.A., Rubhin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

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Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.,

Generation and initial analysis of more than 15,000 full-length
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Submitted (29-MAY-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
                                                                                                                                                                                                                                                                                 779 AGCAGAAGGAACTGGGGGCCTGGGGGAGGATGCCAACGCCGAGGAGGAGGAGGAGGTG
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                          GCAAGAGGCTCCTGGATTATAGCCTGCACAAGGAGGAGGGCCGGCAGCAATCGATTTGCCA
                                                                                                        425 AGGGTATGTCGGAGACCTTTGAGACGCTGCACAACCTAGTCCACAAAGGGGTCAAGGTGG
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AX464002
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NIH-MGC Project URL: http://mgc.nci.nih.gov
On Aug 19, 2003 this sequence version replaced gi:14286319.
Contact: MGC help desk
Email: cgapbs=r@mail.nih.gov
Tissue Procurement: ATC
CDN Library Preparation: Rubin Laboratory
CDN Library Preparation: Rubin Laboratory
CDN Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadanaesystemsbiology.org
contact: amadanaesystemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
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Pred. No. 1.9e-158;
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Best Local Similarity 84.5%;
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Submitted (01-AUG-2003) Department of
Inc., 1 DNA Way, South San Francisco,
Location/Qualifiers
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PRI 03-0CT-2003

AY358960 1675 bp mRNA linear PRI 03-OCT-Homo sapiens clone DNA88004 CTG4A (UNQ1934) mRNA, complete cds. AY358960 GI:37183037

DEFINITION ACCESSION VERSION

Hominidae; Homo.

It (bases 1 to 1675)

Is clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J., Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B., Dowd,P., Eaton,D., Foster,J., Griffinaldi,C., Gu,Q., Hass,P.E., Haldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S., Lee,J., Lewis,L., Limo,P., Mark,M., Robbie,E. Sanchez,C., Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V., Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wieand,D., Kie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z., Goddard,A., Wood,W.I. and Godowski,P.

The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: A Bioinformatics Assessment IPSKCEVCKYVAVELKSAFEETGKTKEVIGTGYGTLDDGASGVKTKSDLRILEVVR
IPSKCEVCKYVAVELKSAFEETGKTKEVIGTGYGTLDDGASGVKYTKSDLRILEVTET
ICKRLIDYSLHKERTGSNRFAKGMSETFETLHNIVHKGVKVMDIPYELMNETSAEVA
DLKKQCDVLVEEFEEVIEDMYRNHQEEDLTEFLCANHVLKGKDTSCLAEQMSGKKGDT
AALGGKKSKKKSSRAKAAGGRSSSSKQRKELGGLEGDPSPEEDEGIQKASPLTHSPPD
EL" translation="MDSMPEPASRCLLLLLLLLLLLLLLLPPELGPSQAGAEENDWVR" 346 124 406 184 466 244 526 304 64 Homo sapiens (human) Homo sapiens Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Bioinformatics, Genentech, CA 94080, USA 185 GATTGCCCAGCAAATGCGAAGTGTGCAAGTATGTTGCTGTGGAGCTGAAGTCGGCTTTTG 245 AGGAAACGGGAAAGACCAAGGAAGTGATTGACACCGGCTATGGCATCCTGGACGGGAAGG cecesaagaaaccecccesrccrrragesrccesecceseccesceareaa TGTCTGAGCTCGCGCCCCCTCTTATTTCCTTTGCTGCTGCTGCTTCCGCTGCTGC 347 recereadecedecedecederererrerrecrirerrecerrecrecrecrecrecre TCCTTCCTGCCCCGAAGCTAGGCCCCGAGTCCCGCCGGGGCTGAGGAGACCGACTGGGTGC CGAGGGAGGAAGCGCCGCCGGCTCCGCTCTGCGTCCGGCTGGGCCATGGAGTCCA Gaps . 9 Length 1675; Indels Score 691.6; DB 8; Pred. No. 1.9e-158;); Mismatches 139; 467 527 g ద 8

us-09-696-686-47.rge

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/trānslation="MDSMPEPSRCLLLLPLLLLLLLLLPAPELGPSQAGAEBNDWVR
LPSKCEVCKYVAVELKSAFBETGKTKEVIGTGYGILDQKASGVKTTKSDLRLIEVTET
ICKRLLDYSLHKERTGSNRFAKGMSETFETLHNLVHKGVKVVMDIPYELMNETSAEVA
DLKKQCDVLVEEFEEVIEDWTRNHQEEDLTEFLCANHVLKGKOTSCLAEQWSGKKGDT
AALGGKKKKKKSSRAKAAGGRSSSSKQRKELGGLEGDPSPEEDEGIQKASPLTHSPPD
BL"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          info@bcggc.bc.ca
Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,
Steve Jones, Sarah Barber, Malliam Chow, Alison Cloutier, Ruth
Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth
Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin,
Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prahbu,
Tarka Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prahbu,
Parvaneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skalska,
Duane Smailus, Jeff Stott, Miranda Tsai, George Yang, Jacquie
Schein, Asim Siddiqui, Rob Holt, Marco Marra.
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (12-MR-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
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cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
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/db_xref="taxon:9606"
/clone="MGC:3530 IMAGE:2819660"
/tiswe type="Lung, small cell carcinoma"
/clone lib="NXH MGC 7"
/lab_mst="DH10B-R"
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/codon start=1
/product="trinucleotide repeat containing
/protein_id="AAH04423.1"
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Contact: MGC help desk
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Pred. No. 1.9e-158;
0; Mismatches 139;
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/db_xref="GeneID:10695"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
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Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
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humanezons or transcripts, for detecting expression and other uses
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Patent: WO 02068579-A 2467 06-SEP-2002;
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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812

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Bukaryota, Metazoa, Chordata, Crandata, Vertebrata, Buteleostomi, Mammalia; Eutheria, Buarchontoglires; Glires; Rodentia; Buteria, Murcidea, Muridae; Murinae; Rattus.

Sciurognathi, Murcidea, Muridae; Murinae; Rattus.

1 (bases 1 to 24640)

8 Marny, D.Marie. Metzker M.Lee., Abrancon, S., Adama, C., Alder, J., Allen, C., Allen, H., Alsbrooks,S., Amin,A., Angulamo, D., Allen, H., Bardaranake, D. Barber,M. Barststead, Benahmed,F., Bladwin,D., Bladrachanake,D. Barber,M. Barststead, R., Ender, M., Calderon,B., Cardera, V., Carter, R., Carderon,B., Cracera, V., Carter, C., Cockell,S., Chen G., Chen R., Chen,Y., Caheror,B., Chen,Z., Chu,J., Clacko,J., Chavez,D., Chen G., Chen R., Chen,Y., Caheror,B., Daylad.O., Denson,S., Derson,C., Ding,Y., Dinh,M., Divyak, M., Deladado,O., Denson,S., Derson,C., Ding,Y., Dinh,M., Divyak,R., Badado,O., Denson,S., Derson,C., Ding,Y., Dinh,M., Divyak,R., Faladado,O., Denson,S., Derson,C., Ding,Y., Padago,M., Foster, P. Fraear,C.M., Gabisi,A., Garne,T., Garne,C., Hanyey,M., Hadan,S., L., Hadan,S., M., Garcia,A., Garner,T., Garza,M., Gebregeorgis,B., Geer,K., Gill,R., Garcia,A., Garner,T., Garza,M., Garcia,A., Havalak,P., Hawes,A., Hume,J., C., Hamilton,C., Hamilton,C., Jacob,L., Jaday,H., Lowan,J., Liu,M., Malloy,K., Maylak,P., Hawes,A., Hume,J., C., Hanges,M., Havalak,P., Hawes,A., Hume,J., Luix,M., Malloy,K., Maylak,P., Hawes,A., Hume,J., Luix,M., Malloy,K., Maylak,P., Maylak,P., Hawes,A., Martin,R., Lui,W., Milladarthe,M., Malladarthe,M., Malloy,K., Martin,R., Maylak,P., Mares,A., Martin,R., Ma
                                                                                                                                                                                                                                                                                                                                                                                                 ALISIBB7 246404 bp DNA linear HTG 09-MAY-2003 Rattus norvegicus clone CH230-3M14, WORKING DRAFT SEQUENCE, 3 UNDOCCERE Dieces.
                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CCAAGGGCATGTCAGAGACCTTTGAGACATTACACAACCTGGTACAAAGGGGTCAAGG
                                                                                               <u> AGAAGCAGTGTGACGTGCTGGTGGAAGAGTTTTGAAGAGGTGATTGAGGACTGGTACAGGA</u>
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HTG; HTGS_PHASE1; HTGS_FULLTOP.
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Rattus norvegicus
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LPSKCEVCKYVAVELKSAFEETGKTKEVIGTGYGILDQKASGVKYTKSDLRLIEVTET
ICKRLLIIACTRRGPAAIDLPRACQRPLRHYTTWYTKGSRW"
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                                                                    Hominidae, Homo.

1 (bases 1 to 962)

Margolis R.L., Abraham,M.R., Gatchell,S.B., Li,S.H., Kidwai,A.S.,
Breschel,T.S., Stine,O.C., Callahan,C., McInnis,M.G. and Ross,C.A.

CDNAs with long CAG trinucleotide repeats from human brain
Hum. Genet. 100 (1), 114-122 (1997)
                                                                                                                                                                                                                                  2 (bases 1 to 962)
Margolis, R.L., Abraham, M.R., Gatchell, S.B., Li, S.H., Kidwai, A.S.,
Breschell, T.S., Strine, O.C., Callahan, C., McInnis, M.G. and Ross, C.A.
Direct Submission
Submitted (02-DEC-1996) Psychiatry, Johns Hopkins Univ. Sch. of
Med., 600 N. Wolfe Street, Meyer 2-181, Baltimore, MD 21205, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          422 CCAAGGGTATGTCGGAGACCTTTGAGACGCTGCACCAACCTAGTCCACAAAGGGGTCAAGG 481
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                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                 1. .962
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            188. .819
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/note="wgs_contig"
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/note="wgs_contig"
188569. .188668
/estimated_length=unknown
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                                                                                                                                                                                                                                                                                                                                                                                Submitted (199-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On May 9, 2003 this sequence version replaced gi:23270097.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html). NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                            Rat Genome Sequencing Consortium.

Direct Submission
Submission
Submitted (27-MUG-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
Baylor Plases 1 to 246404)
Rat Genome Sequencing Consortium.
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------ Summary Statistics
Assembly program: Atlas;
Consensus quality: 230268 bases at least Q40
Consensus quality: 240099 bases at least Q30
Consensus quality: 241516 bases at least Q20
Estimated insert size: 243977; aum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczyk, R., Wooden, H., Worley, K., Wright, D., Wright, P., Wu, J., Yaku, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, X., Zhou, X., Zhou, X., Zhou, X., Zhou, X., Meiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.

Unpublished
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161357: gap of unknown length
188568: contig of 27211 bp in length
188668: gap of unknown length
246404: contig of 57736 bp in length.
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Web site: http://www.hgsc.bcm.tmc.edu/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: hgsc-help@bcm.tmc.edu
------ Project Information
Center project name: GBSQ
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161358. .163910
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/db_xref="taxon:10116"
/clone="CH230-3M14"
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                                                                                                                    663 CACGAGTTGCCTAGCAGAGCGGTGGTCTGGCAAGAGGGGGACATAGCCTCCCTGGGAGG
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Length 246404;
                                                           Indels 101;
  26.3%; Score 484; DB 14; 73.9%; Pred. No. 1.7e-107; iive 0; Mismatches 215;
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Qy 526 GAGGTGGCTGACCTCAAGAAGCAGTGTGACGTGCTGGTGGAAGAGTTTGAAGAGGTGTT 585 bb 361 GAGGTGGCTGACCTCAAGAAGCAGTGTGAAGAGTTTGAAGAGTTTTGAAGAGTGTTC 420 Qy 586 GAGACTGGTACAGGAACCACAGGAGAAGACTGACTGAATTCCTCTGTGCCAACCAC 648 bb 421 GAGGACTGGTACAGGAACACCACAGGAGACTGACTGACTG	Db 661 CCCGAGGAGGATGAGGCATCCAGAAGGCATCCCCTCTCACACACA	JOURNAL Parent: US 6607879-A 274 19-AUG-2003; Incyte Corporation, Palo Alco, CA FEATURES Location/Qualifiers Source 11534 /organism="unknown" /mol_type="genomic DNA" ORIGIN Query Match Best Local Similarity 84.8%; Pred. No. 2.8e-101; Matches 525; Conservative 0; Mismatches 92; Indels 2; Gaps 2;	
Db 24146 TITGGTITGGTICTTGGGTCCTCTCAGAGTGCCCCCTCCCATGTCCTTTTC 24205 Qy 1592 TGCCTTTGTCCCCCAATCCCAGGGGCTGAAGGCCATCACCATGAGGCTTAAC 1649 Db 24206 TGCCTATGTCCCCCAAGTCCAGGAAGGCTGTCATTGAGGGTTAAC 24265 Qy 1650 TGCTATACTACAGAGGTGCTGGAAGGCTCTCATTGAGAGGTTGATT 1692 Db 24266 CTGCTAGTTACTAGAGAGGACAGGTGCCTTCTAGAGCCCCGGGGGGGG	RESULT 12 AR379595 LOCUS LOCUS LOCUS BEQUENCE 140 from patent US 6607879. AR379595 AR379595 AR379595 AR379595 AR379595. GI:40087229 KEYWORDS SOURCE ORGANISM Unclassified. Unclassified. Unclassified. Locations for the detection of blood cell and immunological AUTHORS COCKS, B.G., Stuart, S.G. and Seilhamer, J.J. TITLE COMPOSITIONS for the detection of blood cell and immunological AUTHORS TITLE COMPOSITIONS for the detection of blood cell and immunological Location; Palo Alto, CA FEATURES Incyte Corporation; Palo Alto, CA FEATURES Incyte Corporation, Palo Alto, CA FEATURES Incyte	ORIGIN Query Match Query Match Query Match Best Local Similarity 79.0%; Pred; No. 2.4e-103; Matches 612; Conservative 0; Mismatches 95; Indels 68; Gaps 2; Qy 228 GCTGAAGTCGGCTTTTGAGGAAAGGGAAAGACCAAGGAAGTGATTGACACCGGCTATGG 287	

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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Submitted (22-MAY-2001) National Institutes of Health, Mammalian
Submitted (22-MAY-2001) Cancer Genomics Office, National Cancer
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                   TTGCAAGAGGCTCCTGGATTATAGCCTGCACAAGAAGAAGGACCGGCAGCAATCGATTTGC
                                                                                                               TGAGGAAACCGGCAAGACCAAGGAGGTGATTGGCACGGGCTATGGCATCCTGGACCAGAA
                       GGGCTCTGGAGTCAAGTACACCAAGTCGGACTTACGGTTAATTTGAAGTCACTGAGACCAT
                                    TTGCAAGAGGCTTCTGGACTACAGCCTGCACAAGGAGAGGACTGGCCAGCAACCGGTTTGC
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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AUTHORS
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COMMENT
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 19 Row: n Column: 9.
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cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gontact: amg@bcm.tmc.edu
Gontact: amg@bcm.tmc.edu
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTACGGTTAATTGAAGTCACTGAGACCATTGCAAGAGGCTTCTGGACTACAGCCTGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               694 AAGAAGGGGGACATAGCCTCCCTGGGAGGAAGAAATCCAAGAAGAAGCGCAGCGGAGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAGGAGAGACTGGCAACCGGTTTGCCAAGGGTATGTCGGAGACCTTTGAGACGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CACAACCTAGTCCACAAAGGGGTCAAGGTGGTGATGGATATCCCCTATGAGCTGTGGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cacaaccregiacacaaaaaaaacarcaaacarcaarcaacarccararcaacrerardaaac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       274 GACACCGGCTATGGCATCCTGGACGGGAAGGGCTCTGGAGTCCAAGTACACCAAGTCGGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               413 GAGACTICTGCAGAGGTGGCTGACCTCAAGAAGCAGTGTGATGTGCTGGTGGAAGAGTTTT
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                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="maxna"
/db_xref="taxon:9606"
/clone="Inface:1457829"
/tissue_type="Cervix, carcinoma"
/clone_lib="wall MGC_12"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 457.8; DB 8;
Pred. No. 4.4e-101;
0; Mismatches 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                         organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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Gaps

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333

453 654 513 714 573 774 633

594

834

894 753 954 807

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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

LOCUS DEFINITION

RESULT 15 BC011767

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334 TTACGGTTAATTGAAGTCACTGAGACCATTTGCAAGAGGCTTCTGGACTACAGCCTGCAC 393.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 475 gagccaggccggagcrgaggagagacgacrggrricgccrgccagcaaagggac
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This clone was selected for full length sequencing because ipassed the following selection criteria: Similarity but not identity to protein.
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                                                                                                                                                                                                                                                                                                                                                                                        24.9%; Score 457.8; DB 8; Length ilarity 81.6%; Pred. No. 4.4e-101; Conservative 0; Mismatches 117; Indels
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he : 9087 secs
                                                                                                                                  /organism="Homo sapiens"
                                                                                Location/Qualifiers
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Is (bases 1 to 1533)

Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shemmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Haieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Morley,K.C., Hale,S., Garcia,A., McBwan,P.J.,
Worley,K.C., Hale,S., Garcia,M., Gay,L.J., Hulyk,S.W.,
Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse conn. May 1989.
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Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Mastello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McClowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 27 Row: f Column: 20
                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                        ביטטר 1593 bp mRNA linear PRI 25-JUN-20
Homo sapiens trinucleotide repeat containing 5, mRNA (cDNA clone
PAMGE:3609644), partial cds.
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Submitted (30-UUL-2001) National Institutes of Health, Mammalian
Submitted (30-UUL-2001) Cancer Genomics Office, National Cancer
Gene Collection (MCC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NSC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
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On Dec 19, 2003 this sequence version replaced gi:15079962.
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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BC011767.2 GI:40226374
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REFERENCE AUTHORS TITLE JOURNAL

REMARK COMMENT

PUBMED JOURNAL

TITLE

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A4805286 DNA seque
Adv67441 Nucleotid
Aca54677 Human Nr-
Adu83175 Human CN1
AA821311 Human CDN
ACA61862 BDNA enco
ACA61862 Human Sec
ACA64091 Human CDN
AGA1875 Human PRO
AGA18735 Human PRO
AGA18735 Human PRO
AGA18735 Human PRO
AGA18736 CONA enco
AGA86136 Novel hum
AGD27684 CDNA enco
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AGA86137 Human PRO
AGA15727 Human PRO
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AGA15731 Human PRO
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GenCore version (c) 1993 - 2005
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Maximum Match 100%
Listing first 45 summaries
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Trinucleotide repeat protein; TRP; T243; embryonic stem cell; ES; transgenic animal; knockout mouse; triplet repeat expansion; fragile X syndrome; Huntington's disease; mouse; murine; ss.

Location/Qualifiers

Mus sp. Key /product= "TRP"

WO200130798-A1.

03-MAY-2001

55. .885 /*tag= a 26-OCT-2000; 2000WO-US029382.

99US-0161488P

26-OCT-1999;

Murine trinucleotide repeat protein (TRP) cDNA sequence.

07-SEP-2001 (first entry)

AAS05278;

Novel transgenic animals useful as animal model for characterization of function of a gene encoding trinucleotide repeat proteins (TRPs), contains heterozygous disruption in a gene encoding TRP.

Claim 8; Fig 11; 106pp; English

Allen KD;

Moore M,

(DELT-) DELTAGEN INC. Klein R, Matthews W,

WPI; 2001-300473/31. P-PSDB; AAU02498.

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Cells comprising a heterozogous merings of producting a knockout cells comprising a heterozogous merings of producting a knockout mouse comprising a heterozogous disruption in a target DNA sequence (preferably gene T243) encoding a TRP and of producing a knockout mouse comprising a homozogous disruption in a gene encoding TRP, where the disruption inhibits the production of the wild type TRP. The invention also relates to identifying agents capable of affecting a phenotype of a knockout mouse. Also described are methods of determining whether expansion of the trinucleotide repeat in a gene encoding TRP produces a phenotypic change. The transgenic animals and the cells are useful for identifying compounds capable of ameliorating disease symptoms, and as test substrates for the identification of drugs, pharmaceuticals, therapies and interventions which may be effective in treating trinucleotide repeat disorders are ideal model systems to study the progression of disease in vivo, the molecular medal systems to study the progression of disease in vivo, the molecular basis of these diseases and show the features observed in human disease. Using the mice, it is possible to model both the pathogenic mechanism and the trinucleotide repeat instability in the mouse embryonic stem (ES) trinucleotide repeat protein describes methods of producing present sequence encodes for). The invention describes me

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Sequence 1839 BP; 424 A; 522 C; 535 G; 358 T; 0 U; 0 Other;

240 240 420 540 540 120 120 180 180 300 300 360 360 420 480 480 900 900 99 099 720 720 9 GGCACGAGGGAGGAGCGCCGGCTCCGCTCTGCTCTGGGTCCGGCTGGGCCATGGGAG TCCATGTCTGAGCTCGCGCCCCGCTGCTTATTTCCTTTGCTGCTGCTGCTTCCGCTG TCCATGTCTGAGCTCGCGCCCCCGCTGCTTATTTCCTTTGCTGCTGCTGCTTCCGCTG CTGCTCCTTCCTGCCCCGGAAGCTAGGCCCGAGTCCCGCCGGGGGCTGAGGAGACCGACTGG CTGCTCCTTCCTGCCCCGAAGCTAGGCCCGAGTCCCGCCGGGGCTGAGGAGAGACGACTGG GTGCGATTGCCCAGCAAATGCGAAGTGTGCAAGTATGTTGCTGTGGAGCTGAAGTCGGCT GTGCGATTGCCCAGCAAATGCGAAGTGTGCAAGTATGTTGCTGTGGAGCTGAAGTCGCCT TITGAGGAAACGGGAAAGACCAAGGAAGTGATTGACACCGGCTATGGCATCCTGGACGGG Tricadgaaaceegaaagaccaaegaacigarigacaceegecrafeecarecigeacee AAGGGCTCTGGAGTCAAGTACACCAAGTCGGACTTAACGGTTAATTGAAGTCACTGAGACC AAGGGCTCTGGAGTCAAGTACAAGTCGGACTTACGGTTAATTGAAGTCACTGAGACC ATTTGCAAGAGGCTTCTGGACTACAGCCTGCACAAGGAGAGAGTGGCAGCACCGGTTT ATTTGCAAGAGGCTTCTGGACTACAGCCTGCACAAGGAGGAGGAGGACTGGCAACCGGTTT GCCAAGGGTATGTCGGAGACCTTTGAGACGCTGCACAACCTAGTCCACAAAGGGGTCAAG GCCAAGGGTATGTCGGAGACCTTTGAGACGCTGCACAACCTAGTCCACAAAGGGGGTCAAG GTGGTGATGGATATCCCCTATGAGCTGTGGAACGAGACCTCAGCAGAGGTGGCTGACCTC GTGGTGATGGATATCCCCTATGAGCTGTGGAACGAGACCTCAGCAGAGAGGTGGCTG AAGAAGCAGTGTGACGTGGTGGAAGAGTTTGAAGAGGTGATTGAGGACTGGTACAGG AACCACCAGGAGGAAGACCTGACTGAATTCCTCTGTGCCAACCACGTGCTGAAGGGAAAG AACCACCAGGAGGAAGACCTGACTGAATTCCTCTGTGCCAACCACGTGTGAAGGGAAAG GACACGAGITGCCTAGCAGAGCGGTGGTCTGGCAAGAGGGGGGACATAGCCTCCCTGGGA GACACGAGTTGCCTAGCAGAGCGGTGGTCTGGCAAGAAGGGGGACATAGCCTCCCTGGGA Gaps ö DB 4; Length 1839; 0; Indels 100.0%; Score 1839; 100.0%; Pred. No. 0; ive 0; Mismatches Query Match
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781	CAGAGGAAGGAACTGGGGGGCCTGGGGGGAGGATGCCAACGCCGAGGAGGAGGAGGAGGGTGTG	840
841	CAGAAGGCATCGCCCTCCCACACAGCCCCCTGATGAGCTGTGAGCCCAGCTTAGTGTC	006
901	CTTGAATCAAGACCCCTGACTTCAGAGCTTGGGACACGCGCAGCGCAGCGCAGCGCAGCTCTTGATCATAGAACTTGGGACACCACGCACAGCGCAGCGCAGCCTAGAACTTGGGAACACCACACCACAGCGCAGCGCAGCCAGC	096
961	961 CCAGCAAGGACAGCTGCTGTCCAGCATCAGGTCTCCTCCCTTGGCTGTGCCCCTTTCCTT 102 	1020
1021	CCCTIGAACAACAGCAAGAGGAGGATCIGGGGTGCIGGGAGACGGCACCCCAAAGG 	1080
1081	GAAGAGGAGGAGGAGCAGCACTCTTTTTACACAGTCCCCCTCACGAGCTCCGGGGTTCTCACGAGGAGGAGGAGGAGGAGGAGCAGCTCTTTTTACACAGTCCCCCTCACGAGCAGAGCAGCAGCTCTTTTTACACAGTCCCCCTCACGAGCTCCGG	1140
1141	GGTCCACCCAGCATCCCCAGGCTGAGATCCAGGCTCCTGACATGGAAGCTGAAGAGCATG 	1200
1201	AGGCACATAAGATGCTCACCAGCGCCCCTTCAGCCAGGAAGGA	1260 1260
1261	CAGCCAGGCCTGCTCTTCCTTCCACCAAGCATTCTCTTCTGCTGGTCCTTGTCGGATGG	1320 1320
1321	TAAATTCGAGAACTTCCAGGACAAACTCGGGTGTGGCACAAAGGGGCTGGACGCCAGAGC 	1380 1380
1381	CAGAGCCACGCCAGAGACTGCAGAGAGCACCTGACCTAACCCCCCTGGAAAGCCAATC	1440
1441	TGCAGTTCCCGTGTCCACCCACTCCTCGAGGACGCCTCATGCTCTGCCCAGCCCTTCT	1500
1501	CCCAGGGCTACCAGAGTAAACACCTTTTGGCCTTTCGGTTTGGTTCCTGGGTCCTCATCA	1560 1560
 1561	GCCTCCAGAGTGTCCCCTCATCGATCTTTTTGCCTTTGTCCCCCAATCCCAGGGGCTGG 	1620 1620
1621	AAGGCCATCACCATCATTGGAGGCTTAACCTGTCAGTTACTAGGAGGTGCTGGGAGCGCCC	1680 1680
1681	CGGGGTTGGTTTGGGGTAATCACTCACTGGCTCTCAGCCTTCTAACACTGCAGCCCTTA 	1740
1741	ATACAGITCCTTCTGTTGTGGTGACTCCCACGCCCCCACACACACAC	1800

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gene. The T243 gene encodes for a trinuclectide repeat protein (TRP). The
invention describes methods of producing embryonic stem (ES) cells

comprising a heterozygous disruption in a target DNA sequence (preferably

comprising a heterozygous disruption in a target DNA sequence (preferably

comprising a heterozygous disruption in a gene encoding TRP, where the disruption

inhibits the production of the wild type TRP. The invention also relates

conidentifying agents capable of affecting a phenotype of a knockout

mouse. Also described are methods of determining whether expansion of the

trinucleotide repeat in a gene encoding TRP produces a phenotypic change.

The transgenic animals and the cells are useful for identifying compounds

capable of ameliorating disease symptoms, and as test substrates for the

identification of drugs, pharmaceuticals, therapies and interventions

which may be effective in treating trinucleotide repeat disorders e.g.

fragile X syndrome and Huntington's disease. The animal models for

trinucleotide repeat disorders are ideal model systems to study the

progression of disease in vivo, the molecular basis of these diseases and

show the features observed in human disease. Using the mice, it is

possible to model both the pathogenic mechanism and the trinucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel transgenic animals useful as animal model for characterization of function of a gene encoding trinucleotide repeat proteins (TRPs), contains heterozygous disruption in a gene encoding TRP.
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Pred. No. 0;
                                                                                                                                                                                     Trinucleotide repeat protein; TRP; T243; embryonic stem cell; transgenic animal; knockout mouse; triplet repeat expansion; fragile X syndrome; Huntington's disease; mouse; mutant; ds.
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Allen KD
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                                                                                                                                                               DNA sequence of an expanded T243 gene.
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96.6%;
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/*tag= a /*tag= a /product = "protein involved in FGF signal transduction"
        CCCCAAAGGGAAGAGGAGGAGGAGCAGCAGCTCTCTTTCTACACAGTCCCCCTCAC
                   CCCCAAAGGGAAGAAGGAGGAGGAGCAGAAGGCAGCTCTCTTTCTACACAGTCCCCCTCAC
                                          GAGCTCCGGGGTCCACCCAGCATCCCCAGGCTGAGATCCAGGCTCCTGACATGGAAGCTG
                                                     CAGCCTCAGCCAGGCCTGCCTCTTCCTTCCACCAAGCATTCTCTTCTGCTGGTCCTT
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The present sequence encodes a protein involved in fibroblast growth factor (FGF) signal transduction. Such proteins are useful for analyzing the mechanism of formation of various organs, such as midbrain opticatetum portion by a midbrain mesencephalon border, the mechanism of formation of cerebellum. mechanisms of formation of inner ear, blood vessels, limb buds, teeth, and canceration mechanisms of a cell.
                                                                                                                                                                                                                                                                                                                                                                                    Novel gene encoding protein involved in fibroblast growth factor signal transduction, useful for analyzing mechanism of formation of organs such as midbrain optic-tectum portion, cerebellum, inner ear and canceration mechanism of cell.
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Ammuniani uncrear lacturing proposed in the proposed in the control of the contro Novel NF-kappaB-associated polypeptides and polynucleotides useful for disgnosing, treating and preventing cancer, hepatic disorders, aberrant apoptosis, viral infections, autoimmune disorders, asthma and stroke. cancer; nuclear factor-kappaB; NF-kappaB; immune disorder; Human NF-kappaB associated polynucleotide sequence #117 Claim 4; Fig 10H; 608pp; English (BRIM) BRISTOL-MYERS SQUIBB CO. Carman J, Feder J, Nadler S; 19-APR-2001; 2001US-0284962P. 26-APR-2001; 2001US-0286645P. 09-JAN-2002; 2002US-0346986P. 19-APR-2002; 2002WO-US012636 WPI; 2003-093119/08. P-PSDB; ABU69616 WO200286076-A2. Homo sapiens 31-OCT-2002

The present invention relates to the isolation of human nuclear factorkappaB (NP-kappaB) associated polypeptides and polynucleotides. The NPkappaB associated polypeptide and polynucleotide sequences are useful for
preventing, treating or ameliorating various disorders including immune
disorders, inflammatory disorders, cancers, disorders relating to
aberrant apoptosis, hepatic disorders, Hodgkin's lymphomas,
concern apoptosis, hepatic disorders, Hodgkin's lymphomas,
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ACA54677 standard; cDNA; 1378 BP ACA54677 RESULT 4 ACA54677

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                                                                    Score 691.6; DB 10;
Pred. No. 6.4e-168;
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                                                                            Query Match
Best Local
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Nuclear factor kappa B; NFkappaB; inflammation; cardiovascular disease; neoplasm; gastrointestinal disease; immune disorder; immune deficiency; dermatological disease; infection; nutritional disorder; imforder; cerebrovascular ischemia; endocrine disease; injury; respiratory disease; gynecology and obstetrics; kawasaki disease; rheumatic fever; diagnosis;
                                             Human trinucleotide repeat containing 5 protein, cDNA.
       BP.
       ADU83175 standard; cDNA; 1378
                                                                                                                                                           07-MAY-2003; 2003US-00431096.
                                                                                                                                              06-MAY-2004; 2004WO-US014279.
                                 (first entry)
                                                                                                                    WO2004100886-A2
                                                                                                       Homo sapiens.
                                 10-FEB-2005
                                                                                                                                  25-NOV-2004.
                                                                                          gene.
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New nucleic acid molecule encoding an NFkappaB associated molecule, useful for diagnosing, preventing, treating, or ameliorating a medical condition, e.g. cancer, wounds, or immune, inflammatory, hepatic, viral or pulmonary disorder.

8

(BRIM) BRISTOL-MYERS SQUIBB

Nadler SG;

Carman J, Feder JN, 2005-047909/05. P-PSDB; ADU83186 Claim 1; SEQ ID NO 139; 646pp; English.

The invention relates to an isolated nucleic acid molecule having

NEKARAPABE (nuclear factor kappa B) modulating activity (or its fragments,

ariants, homologs and sequences hybridizing to it). Also included are an

isolated polypeptide capable of modulating an NFkappaB response (or its

domain, epitope, variant, species homolog or interacting protein), an

isolated antibody that binds specifically to the isolated polypeptide, a

method for preventing (treating, or ameliorating) a medical condition, a

method of diagnosing a NFkappa associated condition (or a susceptibility

to a NFkappaB associated condition) in a subject, a method of identifying

a compound that modulates the biological activity of a NFkappaB

associated molecule, a method of screening for a compound that is capable

of modulating the biological activity of a NFkappaB

associated molecule as identified by any of the methods above. The

anceleic acid molecule as identified by any of the methods above. The

condition, e.g. immune disorder, an inflammatory disorder in which

condition, e.g. immune disorder, an inflammatory disorder related to

condition, e.g. immune disorder, an inflammatory disorder related to

aberrant NFkappaB regulation, a cancer, aberrant apoptosis, hepatic

condition, e.g. immunedeficiency, an inflammatory disorder related to

aberrant NFkappaB regulation, a cancer, aberrant apoptosis, hepatic

disorders, Hodgkins lymphomas, hematopoietic tumors, hyper-IgM syndromes,

HYD-1, HTM-1, HTM-1, hepatitis B, hepatitis C, EBV, influenza, viral

confliction, e.g. immunedeficiency, and inflammatory viral infections,

creplication, host cell survival, and evasion of immune responses. rheumatoid arthritis, inflammatory bowel disease, colitis, asthma, atherosclerosis, cachexia, euthyroid sick syndrome, stroke, BAE, autoimmune disorders disorders disorders instanced to hyper immune activity, disorders related to aberrant acute phase responses, hypercongenital conditions, birth defects, necrotic leaions, wounds, organ transplant rejection, conditions related to organ transplant rejection, disorders related to aberrant signal transduction, proliferating disorders, HIV

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propagation in cells infected with other viruses, associated with EL-8, disorders associated with aberrant IL-8 expression, disorders associated with aberrant IL-8 activity, pulmonary disorders, pulmonary fibrosis, Behcet's disease, bacterial infections, growerological diseases, psoriasis, IgA nephropathy, chronic obstructive pulmonary disease, Kawasaki disease, Crohn's disease, peripheral arterial occlusive disease, Hodgkin's disease, idiopathic intermediate uveitis, hyaline membrane disease, acute rheumatic fever, chronic rheumatic heart disease, ulcerative colitis, autoimmune disorders, and autoimmune thyroid disease. The present sequence encodes a protein found to interact with the NFkappa
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                                                                                                                                                                                                                                                                                         Sequence 1378 BP; 311 A; 399 C; 419 G; 249 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                     / Match 37.6%; Score 691.6; DB 14; Local Similarity 84.5%; Pred. No. 6.4e-168; nes 791; Conservative 0; Mismatches 139;
                                                                                                                                                                                                                                               modulating protein AD037
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                                                                                                                                                                                                                                                                                                                                          Query Match
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Matches
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Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte; A-peptide; factor VIIA; gene therapy; ss.
                                                                                                                                 Human cDNA sequence encoding for PRO4409 polypeptide
                               934
                               TCCTTGAATCAAGACCCCTGACTTCAGAGCTTGGGA
                                        ВР
                                                                                    AAS21311 standard; cDNA; 1675
                                                                                                                                                                                                                                                                                  99WO-US028565.
99US-0170262P.
99WO-US030095.
99WO-US030911.
                                                                                                                                                                                                                                                                                                                 99WO-US030999.
99WO-US031243.
99WO-US031274.
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2000WO-US004414.
2000WO-US004914.
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                                                                                                                   (first entry)
                                                                                                                                                                                                       WO200140466-A2.
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11-FEB-2000;
18-FEB-2000;
                                                                                                                                                                                                                                      01-DEC-2000;
                                                                                                                                                                                        Homo sapiens
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08-NOV-2000;
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02-DEC-1999
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TCCAGAAGGCATCCCCTCTCACACACACCCCCCCTGATGAGCTCTGAGCCCCACCAGCAT 1186
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tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;
differentiation; chondrocyte; tumour; genetic disorder; cytostatic; gene;
                                                                                                                                                                                                                                                                                                           947 CCAGTTGCCTGGCAGAGCAGTGGTCCGGCAAGAAGGGAGAGACACAGCTGCCCTGGGAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1067 AACAAAGGAAGGAGCTGGGTGGCCTTGAGGAGAACCCCCGAGCAGGAGGATGAGGCA
107 AGGGCATGTCAGAGACCTTTGAGACATTACACAACCTGGTACACAAAGGGGTCAAGGTGG
                                                                                   TGATGGACATCCCCTATGAGCTGTGGAACGAGACTTCTGCAGAGGGGGGTGGCTGACCTCAAGA
                                                                                                                                                                                                   779 AGCAGAGGAAGTGGGGGGCCTGGGGGAGGATGCCAACGCCGAGGAGGAGGAGGTG
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                                                                                                                                                                 AGCAGTGTGACGTGCTGGTGGAAGAGTTTGAAGAGGTGATTGAGGACTGGTACAGGAACC
                                                                                                                                                                                                                                                                              ACCAGGAGGAAGACCTGAATTCCTCTGTGCCAACCACGTGCTGAAGGGAAAGGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        725 AGAAATCCAAGAAGAAGCGCAGCGGAGTCAAG-----GGCTCCTCCAGTGGCAGCAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1007 agaagriccaagaagaagaagcagcaagcaagcagcagcagcagaagragcagcagcagcag
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98WO-US018824.
98WO-US019093.
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98WO-US019330.
98WO-US019437.
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98WO-US024855.
98WO-US025108.
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98WO-US022991.
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98WO-US014552
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                                                                                                                                                                                                                                                                                                                                                                                                                                            AAS21244-AAS21518 encode for novel human secretory and transmembrane PRO polypeptides. The PRO polypeptides are useful to detect other PRO polypeptides, to link bioactive molecules to cells expressing PRO polypeptides, to modulate biological activities of cells expressing PRO polypeptides, and to detect the presence of mammalian lung, colon, breast, prostate, rectal, cervical or liver tunours by comparing PRO polypeptide expression in a cell sample to that in a control sample. Some of the 275 sequences are also useful to stimulate the release of tumour necrosis factor alpha (TNF-alpha) from human blood, the proliferation or differentiation of chondrocytes, the proliferation or proliferation of inner ear utricular supporting cells or of the PRO polypeptides may modulate glucose or free fatty acid uptake by skeletal muscle cells or by adipocytes, or the proliferation of endothelial cells. Some of the PRO polypeptides can be used in assays to identify molecules involved in binding interactions. The polymcidenia process encoding PRO polypeptides can be used in assays to identify molecules transgenic or knock out animals and can be used in gene therapy
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                                                                                                                                                                                                                                                    Isolated , secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bioactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumors e.g. lung, breast, prostate, cervical.
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                                                         Deforge L, Desnoyers L, Filvaroff E, G.
1, Godowski PJ, Gurney AL, Sherwood S;
Tumas D, Watanabe CK, Wood WI, Zhang Z;
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                               Baker KP, Beresini M, Deforge L
Gerritsen ME, Goddard A, Godows
Armas D, Tumas D,
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     (GETH ) GENENTECH INC
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P-PSDB; AAU12239
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99WO-US031243
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2001US-00882636
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11-FEB-2000; 2
18-FEB-2000; 2
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08-NOV-2000;
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17-MAY-2000;
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13-SEP-1999;
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The present invention relates to the isolation of novel human PRO
polypeptides, and the polynucleotide sequences encoding them. The PRO
polypeptides are secreted and transmembrane proteins. The PRO
polypeptides are useful for detecting other PRO polypeptides, for linking
polypeptides are useful for detecting other PRO polypeptides, for linking
biological activities of cells expressing PRO polypeptides, and for for
identifying agonists or antagonists. The PRO polypeptides are useful for
contentifying agonists or antagonists. The PRO polypeptides are useful for
the stimulating the release of tumour necrosis factor (TNF)-alpha from
the ploof, for stimulating the proliferation or differentiation of
chondrocytes, and detecting the proliferation or differentiation of
chondrocytes, and detecting the presence of tumours. The polynucleotide
sequences encoding PRO polypeptides are useful as hybridisation probes,
in chromosome and gene mapping, in the generating transgenic
DNA, in the preparation of PRO polypeptides, for generating transgenic
animals or knockout animals, for the generic analysis of individuals with
content of isorders, and in gene therapy. ACA03603-ACA03877 represent cDNAs
encoding the human PRO polypeptides of the invention. Note: The sequence
data for this patent was obtained in electronic format directly from the
USPTO web site at sequate.
                                                                                                                                                                                                                                                                                                                                                                                                                                  New secreted and transmembrane PRO nucleic acids, useful for gene therapy, in chromosome and gene mapping, as chromosome markers, in tissue typing, and in chromosome identification.
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Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
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             20-JUN-2001; 2001WO-US019692.
21-JUN-2001; 2001WS-0088-W19.
22-JUN-2001; 2001WG-US02116.
29-JUN-2001; 2001WO-US02116.
09-JUL-2001; 2001WG-US021735.
18-JUL-2001; 2001US-00908827.
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  1067 AACAAAGGAAGGAGCTGGGTGGCCTTGAGGGGAGACCCCCGAGCCCCGAGGAGGAGGAGGAGA 1126
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587 CCTCTGGAGTCAAATACACCAAGTCGGACTTGCGGTTAATCGAAGTCACTGAGACCATTT 646
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                                   GCAAGAGCTTCTGGACTACAGCCTGCACAAGGAGGAGCTGGCAGCAACCGGTTTGCCA 424
                                                         GCAAGAGGCTCCTGGATTATAGCCTGCACAAGGAGAGGACCGGCAGCAATCGATTTGCCA 706
                                                                               AGGGTATGTCGGAGACCTTTGAGACGCTGCACAACCTAGTCCACAAAGGGGTCAAAGGTGG 484
                                                                                                    AGGCCATGTCAGAGACCTTTGAGACATTACACAACCTGGTACACAAAGGGGGTCAAGGTGG 766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing; cardiac insufficiency disorder; cancer; tumour; immune response; adrenal cortical capillary endothelial growth; c-fos induction; vascular endothelial growth factor inhibition; VBGF inhibition; endothelial cell growth inhibitor; T-lymphocytes stimulation; retinal neurons cell survival; rod photoreceptor cell survival; retinal disorder; retinitis pigmentosum; kidney disorder; mammalian kidney mesangial cell proliferation; Berger disease; dermatitis; herpetiformis; Crohn's disease; chondrocyte proliferation; chondrocyte redifferentiation; sports injury; arthritis; gene; ss.
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Claim 2; Fig 135; 659pp; English.
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Gerritsen ME, Goddard A,
Smith V, Stéwart TA, Tum
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3 Gao Deforge L, Desnoyers L, Filvaroff E, G A, Godowski PJ, Gurney AL, Sherwood S; Tumas D, Watanabe CK, Wood WI, Zhang Z;

Two hundred and seventy five nucleic acids encoding PRO polypeptides, useful for treating pericyte-associated tumors, diabetes and various bone and/or cartilage disorders, e.g. arthritis.

The invention describes an isolated human PRO polypeptide. The PRO polypeptides are useful in detecting PRO polypeptides in a sample, in constraint a bioactive molecule to a cell expressing a PRO polypeptide, and in modulating at least one biological activity of a cell expressing a PRO in modulating at least one biological activity of a cell expressing a PRO polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus cusful for treating cardiac insufficiency disorders. PRO154 and PRO136, PRO943, PRO944, PRO944, PRO943, PRO943, Induce the Coreased mesangial cell function such as Berger disease or other comphropathies associated with dermatitis, herpotherican such the reference of injuries, PRO9132, PRO913, and PRO91397 induce the Change of these pro9110, PRO944, PRO9131, PRO913, Induce the Change of these pro9110, PRO944, PRO9131, PRO913, Induce the Change of these pro91 bush propers injuries, and arthritis. This sequence of the proper bush human PRO PROPES. encodes a novel human PRO protein

ACD41862 standard; cDNA; 1675 BP. RESULT 9 ACD41862 ID ACD4:

Sequence 1675 BP; 380 A; 469 C; 520 G; 306 T; 0 U; 0 Other;

245 AGGAAACGGGAAAGACCAAGGAAGTGATTGACACCGGCTATGGCATCCTGGACGGAAGG 304 Aacaaaggaaggraggraggcrargaggagagaccccagccccgaggaggargaggga 1126 346 664 406 TCCTTCCTGCCCCGAAGCTAGGCCCGAGTCCCGCCGGGGGCTGAGGAGACCGACTGGGTGC 184 466 244 GCCTGCCCAGCAAATGCGAAGTGTGTAAATATGTTGCTGTGGAGCTGAAGTCAGCCTTTG 526 364 587 cererecadredadraceceadereceaerrecegrinalecadeceaerecades 424 484 AGGCATGTCAGAGACCTTTGAGACATTACACAACCTGGTACACAAAGGGGTCAAGGTGG 544 TGATGGACATCCCCTATGAGCTGTGGAACGAGACTTCTGCAGAGGTGGCTGACTCAAGA 826 604 827 AGCAGTGTGATGTGCTGGAAGAGTTTGAGGAGGTGATCGAGGACTGGTACAGGAACC 886 779 AGCAGAGGAAGGAACTTGGGGGGCCTGGGGAGGATGCCAACGCCGAGGAGGAGGAGGAGGTG 838 TGCAGAAGGCATCGCCCCTCCCACACCCCCCTGATGAGCTGTGAGCCCCAGCTTAGTG 898 64 TGTCTGAGCTCGCCCCCCCCTCTTATTTCCTTTGCTGCTGCTGCTTCCGCTGCTGC 725 AGAAATCCAAGAAGAAGCGCAGCGAGTCAAG-----GGCTCCTCCAGTGGCAGCAGCA 527 AGGAAACCGGCAAGACCAAGGAGGTGATTGGCACGGGCTATGGCATCCTGGACCAGAAGG GATTGCCCAGCAAATGCGAAGTGTGCAAGTATGTTGCTGTGGAGCTGAAGTCGGCTTTTG 647 GCAAGAGGCTCCTGGATTATAGCCTGCACAAGAGAGGACCGGCAGCAATCGATTTGCCA AGCAGTGTGACGTGCTGGTGGAAGAGTTTGAAGAGGTGATTGAGGACTGGTACAGGAACC CGAGGGAGGAAGCGCCGCCGGGTCCGCTCTGCTCTGGGTCCGGCTGGGCCATGGAGTCCA GCTCTGGAGTCAAGTACACCAAGTCGGACTTACGGTTAATTGAAGTCACTGAGACCATTT <u> AGGGTATGTCGGAGACCTTTGAGACGCTGCACAACCTAGTCCACAAAGGGGGTCAAGGTGG</u> TGATGGATATCCCCTATGAGCTGTGGAACGAGACCTCAGCAGAGGTGGCTGACCTCAAGA ACCAGGAGGAAGACCTGACTGAATTCCTCTGTGCCAACCACGTGCTGAAGGGAAAGGACA . 9 Length 1675; 37.6%; Score 691.6; DB 8; Length 84.5%; Pred. No. 7e-168; ive 0; Mismatches 139; Indels cercrigicercada de cercita de la 1222 de cercrigica de 1222 de cercada de 1222 de cercada de 1222 de cercada decembra de cercada de 899 TCCTTGAATCAAGACCCCTGACTTCAGAGCTTGGGA 934 Query Match 37.6 Best Local Similarity 84.5 Matches 791; Conservative 999 1067 839 1127 1187 Ŋ 287 347 125 407 185 467 305 365 425 707 167 545 65 485 605 g ઠે g ò 셤 ઠે a ò g ò 셤 ò a g ઠ g g ò g g 셤 g 8 ઠ à ò ò ð 셤

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blood;
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                                 Human secreted/transmembrane protein (PRO) cDNA #68.
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14-SEP-1998;
16-SEP-1998;
                                                                                                                                                                                                                17-SEP-1998;
07-OCT-1998;
29-OCT-1998;
29-OCT-1998;
20-NOV-1998;
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                    05-SEP-2003
                                                                                                                                                                                                                                                  01-DEC-1998;
05-JAN-1999;
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10-MAR-1999;
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14-MAY-1999;
                                                                                                                                                                                                                                                                                                                                 05-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                              30-NOV-1999;
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                                                                                                                                                                                                                                                                                                       08-SEP-1999
                                                                                                                             20-FEB-2003
       ACD41862;
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The invention relates to an isolated nucleic acid comprising at least 80 sequence identity to a PRO (secreted and transmembrane protein) cDNA comprising a nucleic acid (a) encoding a PRO polypeptide, or its extracellular domain (with or without its associated signal peptide), which comprises any of the 275 120-850 residue amino acid sequences, given in the specification; (b) comprising any of the 275 300-3500 nucleotide sequences, given in the specification; or (c) comprising the full-length coding sequence of the nucleotide sequences given in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO1114 PRO4978, useful in molecular biology, chromosome and gene mapping, generating antisense RNA and DNA, and in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, G:
Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 2; Fig 135; 659pp; English.
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2000US-00747259.
2000WO-US034956.
2001US-00796498.
2001WO-US006520.
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2001US-00802706
2001US-00808689
2001US-0081844
2001US-00854208
2001US-00854208
2001US-00860216
2001US-00860216
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2001US-00872035.
2001WS-00874503.
2001US-00874503.
2001US-00886342.
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2000WO-US022031.
2000WO-US022031.
2000WO-US023522.
2000WO-US03338.
2000WO-US0330952.
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2001US-00908827.
2001US-00924419.
2001US-00927796.
2000WO-US005746.
2000WO-US005841.
2000WO-US006319.
2000WO-US007377.
2000WO-US007377.
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2000WO-US013705.
2000WO-US014042.
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2001WO-US020116.
2001WO-US021066.
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19-DEC-2001; 2001US-00028072
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P-PSDB; ABO24908.
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24-AUG-2000;
10-NOV-2000;
01-DEC-2000;
20-DEC-2000;
28-FEB-2001;
28-FEB-2001;
01-MAR-2001;
09-MAR-2001;
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14-JUN-2001;
19-JUN-2001;
20-JUN-2001;
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22-JUN-2001;
29-JUN-2001;
                                                                                                                            30-MAR-2000;
17-MAY-2000;
22-MAY-2000;
30-MAY-2000;
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01-JUN-2001;
01-JUN-2001;
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in in

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Specification (ATCC) Accession Numbers listed in the American in per dispersion of ATCC) Accession Numbers listed in the specification.

Also included are a vector comprising the novel nucleic acid, a host cell comprising the vector, producing a RPO polypeptide, the isolated RPO polypeptides detailed above, a chimmeric molecule comprising the PRO polypeptide of fused to a heterologous amino acid sequence, an anti-PRO polypeptide of fused to a heterologous amino acid sequence, an anti-PRO comprising a RPO polypeptide, including at least one biological activity of a cell expressing a RPO polypeptide, stimulating the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, (or proteoglycans from cartilage or cytokine from peripheral blood monouclear cells (PBMC)), andipocyte cells or proliferation of or gene expression in pericyte cells, stimulating the proliferation of rinner ear utricular supporting cells), stimulating the proliferation of rinner ear utricular supporting cells, or of T-lymphocyte cells, or of endothelial cells), inhibiting the binding of A-peptide to factor VITA, or differentiation of adipocyte cells (or of T-lymphocyte cells, or of the polymore in a mammal and an oligonucleotide probe derived from any of the nucleotide sequences given in the specification. The polymore in a mammal and an an oliferation and an an antisense RNA and DNA, and in gene therapy. The combinant techniques, and in generating either transgenic animals or recombinant techniques, and in generating either transgenic animals or recombinant techniques, and in generating either transgenic animals or antibody is used in preparing a medicament for treating a condition and in serious disconting a medicament for treating a condition arranged and an arranged and the propersive or the polymore and second antibody, such animals which, in the preparating a medicament for treating a condition and an arranged and an arranged and an arranged and an arranged and and an arranged and and and an arranged and and an arranged and a
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specification, or of the DNA deposited under any of the American Type
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inflammatory disease; organ failure, atherosoclerosis; cardiac injury;
infertility; birth defects; premature aging; AIDS; biosensor;
acquired immunodeficiency syndrome; cancer; diabetic complication;
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18-JUL-2001; 2001US-00908827. 06-NG-2001; 2001US-00927419. 09-AUG-2001; 2001US-00927796. 16-AUG-2001; 2001US-00931836. 19-DEC-2001; 2001US-00928072. 2001WO-US021735 09-JUL-2001;

(GETH) GENENTECH INC

3 Gao Beresini M, Deforge L, Desnoyers L, Filvaroff E, Ga ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z; Gerritsen ME, Goddard Smith V, Stewart TA, Baker KP,

WPI; 2003-331925/31. P-PSDB; ABU66913.

New secreted and transmembrane nucleic acids and polypeptides, designated as PRO, useful for treating inflammation, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, AIDS, or cancer.

Claim 2; Fig 135; 659pp; English.

The invention relates to an isolated nucleic acid comprising, or which is at least 80% identical to, or the full-length coding sequence of, any of the 27% nucleotide sequences, encoding the corresponding PRO polypeptide (one of 275 secreted or transmembrane proteins). The nucleic acid further comprises the full-length coding sequence of the DNA deposited under the specification. Also included are vectors and host cells for in the specification. Also included are vectors and host cells for producing PRO proteins, PRO tusion proteins, anti-PRO antibodies, PRO extracellular domains and mature sequences, methods of detecting PRO proteins and mature sequences, methods of detecting PRO corresis factor alpha) from human blood, (and the proliferation of corresis factor alpha) from human blood, (and the proliferation of corresis factor alpha) from human blood, (and the proliferation of correction of artilage, proliferation of funct ear urticular supporting cells, the catilage, proliferation of funct ear urticular supporting cells, the correction of activation of any proliferation of function of inner ear urticular supporting cells, the correction of a cytokine from peripheral blood monounclear cells, the release of a cytokine from peripheral blood monounclear cells, the release of a cytokine from correction of T-lymphocyte cells, an eached for modulating the uptake of glucose or free endothelial cells), a method for modulating the uptake of glucose or featured binding of A-peptide to factor VIIA, or the differentiation of adeceting the presence of a tumour in a mammal and olygomucleotide probe derived from any of the nucleotide sequences cells, and polypeptides are useful for treating confidence of immunodeficiency syndrome), cancer, or diabetic complications. The nucleic acids are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. Both concern angelul at pharmaceuticals, diagnostics, biosensors or bioreactors. Both

Sequence 1675 BP; 380 A; 469 C; 520 G; 306 T; 0 U; 0 Other;

346 406 184 rerendaderrececececerecerrarirecrineriecriecriecricecececrise 124 407 TGCTGCCGGCCCGGAGCTGGGCCCGAGCCGGAGCTGAGGAGAACGACTGGGTTC 466 64 347 igccidalaccacarccaciartreracriterreceriacracracracracracracra TCCTTCCTGCCCCGAAGCTAGGCCCGAGTCCCGCCGGGGCTGAGGAGACCGACTGGGTGC CGAGGGAGGAAGCGCCGCCGCTCCGCTCTGGGTCCGGCTGGGCCATGGAGTCCA Gaps 9: 37.6%; Score 691.6; DB 8; Length 1675; 84.5%; Pred. No. 7e-168; ive 0; Mismatches 139; Indels 6; Best Local Similarity 84.5 Matches 791; Conservative Ŋ 65 125 Query Match g 셤 셤 à à ð

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Tumour necrosis factor alpha release; TNF-alpha release;
Jucose uptake modulator;
cell proliferation stimulator; tell differentiation stimulator;
cell differentiation inhibitor; cytokine release stimulator; tumour;
lung tumoue; colon tumour; breast tumour; prostate tumour; rectal tumour;
cervical tumour; liver tumour; chromosome mapping; gene mapping;
gene therapy; chromosome identification; chromosome marker.
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               GCCTGCCCAGCAATGCGAAGTGTGTAATATGTTGCTGTGGAGCTGAAGTCAGCCTTTG
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Novel human secreted and transmembrane protein PRO4409 cDNA.
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(GETH) GENENTECH INC

Gao W; Deforge L, Desnoyers L, Filvaroff E, Ga A, Godowski PJ, Gurney AL, Sherwood S; Tumas D, Watanabe CK, Wood WI, Zhang Z; Baker KP, Beresini M, De Gerritsen ME, Goddard A, Stewart TA, Smith V,

2003-584997/55. P-PSDB; ADA45655

Novel secreted and transmembrane polypeptide for modulating biological activity of cell expressing the polypeptide, identifying agonists or antagonists of polypeptide, and as molecular weight markers.

Claim 2; Fig 135; 659pp; English.

The invention describes 305 nucleic acids encoding PRO (secreted and transmembrane) polypeptides (1). (1) is useful for stimulating the cralesse of TWF-alpha from human blood, for modulating the uptake of glucose or FFA by skeletal muscle cells or adipocyte cells, for glucose or FFA by skeletal muscle cells or adipocyte cells, for stimulating the proliferation of or gene expression in pericyte cells, for stimulating the proliferation of inner ear utricular supporting cells, constimulating the proliferation of T-lymphocyte cells, for stimulating the proliferation of T-lymphocyte cells, for stimulating the proliferation of T-lymphocyte cells, for stimulating the proliferation of function of adipocotic cells, for stimulating the proliferation of endothelial cells, for stimulating the proliferation of endothelial cells, for detecting the presence of tumour in a mammal. The tumour is lung, colon, breast, colls, for simulating genomic and cDNA nucleotide sequences or arrisense probes. (1) is also useful as therapeutic agent. PRO is useful in assays to identify other proteins or molecules involved in binding in assays to identify other proteins or molecules involved in binding in assays to identify other proteins or molecules involved in binding correction. A polynucleotide (II) encoding (I) is useful in the development and correction of PRO polypeptide, for generating transgenic animals which in turn are useful in the development and correcting of therapeutically useful reagents, in gene therapy, for chromosome identification, as chromosome anaker, and for generating chromes identification, as chromosome anaker, and for generating chromesian in specific cells, tissues or serum, and for

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affinity purification of PRO from recombinant cell culture or natural sources. (I) and (II) are useful for tissue typing. This sequence encodes a novel human secreted and transmembrane PRO polypeptide.
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                                                                   Score 691.6; DB 9; Length 1675;
Pred. No. 7e-168;
0; Mismatches 139; Indels 6;
                                               Sequence 1675 BP; 380 A; 469 C; 520 G; 306 T; 0 U; 0 Other;
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Matches 791; Conservative 0
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New isolated nucleic acid encoding a secreted and transmembrane polypeptide, designated e.g. PRO1114 or PRO4978, useful in chromosome and gene mapping, in generating antisense RNA and DNA, and in gene therapy.
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Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
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Human; gene; 88; PRO; secreted polypeptide; transmembrane polypeptide; tummour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tummour; cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular endothelial cell; glucose; FFA; skeletal muscle cell; adipocyte cell; pericyte cell; inner ear utricular supporting cell; T-lymphocyte cell; endothelial cell tube formation; bone disorder; cartilage disorder; sports injury; proteoglycan; articular cartilage defect; osteoarthritis; rheumatoid arthritis; haemoglobin-associated disorder thalassaemia; immune system cell infiltration.
                               ADA76085 standard; cDNA; 1675 BP
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                                                                                  Human PRO polynucleotide #68
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                                                                (first entry)
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07-OCT-1998;
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2001US-00866028.
2001US-00866034.
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2001WG-00872035.
2001WG-00874503.
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2001US-00927796.
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2001US-00796498.
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18-FEB-2000;
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The invention relates to alorated human PKU polypeptides lescreted and transmembrane polypeptides an antibody which specifically binds to a PRO invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour in necrosis factor-alpha (TMF-alpha) from human blood, a method for stimulating the proliferation or differentiation of chondrocyte cells and a method for chordrocyte cells and a method for chordrocyte cells and a method for detecting the presence of a tumour in a mammal (e.g. adrenal, lung, colon, breast, prostate, rectal, kidney, cervical and liver tumours). The polyprucleotides are useful in molecular biology, including uses as inclusioned properties by recombinant techniques and in antisense RNA and DNA and in gene therapy. The polyprucleotides may also activated in preparing PRO polypeptides by recombinant techniques and in antisense there is the ransgenic animals or knock-out animals which are useful in the development and screening of therapeutically useful and edicament for treating a condition responsive to the polypeptides or antibodies are used in preparing a condition responsive to the polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation of or proliferation of or specestal muscle cells, for modulating proliferation of stimulating editocyte cells, for stimulating the upcake of glucose or FRA by skeletal muscle cells or adipocyte cells, for stimulating cheration of adipocyte cells, for stimulating cheration of cartilage disorders such as sports injuries and architics. PRO polypeptides which stimulate the release of prolegylycans (from cartilage are useful for treating sports-related joint problems, arthritis. PRO polypeptides which stimulate edit sorders such as various mammalian haemoglobin-associated disorders such as various thalassaemias and conditions which sequence represents a human PRO polymericed data for this patent is also available in electronic forms formations.
to isolated human PRO polypeptides (secreted and
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Gaps 9 DB 9; Length 1675; Sequence 1675 BP; 380 A; 469 C; 520 G; 306 T; 0 U; 0 Other; Score 691.6; DB 9; Length Pred. No. 7e-168; 0; Mismatches 139; Indels 37.6%; 84.5%; Query Match
Best Local Similarity 84.5'
---hes 791; Conservative

646 994 406 466 244 526 304 586 364 424 484 TGATGGATATCCCCTATGAGCTGTGGAACGAGACCTCAGCAGAGGTGGCTGACCTCAAGA 544 287 cecesesaceaaceacececesrecrriaesereceseceseceseceaecearearrea 346 TGTCTGAGCTCGCGCCCCCGCTGTTATTTCCTTTGCTGCTGCTGCTTCCGCTGCTGC TCCTTCCTGCCCCGAAGCTAGGCCCGAGTCCCGGGGGCTGAGGAGACCGACTGGGTGC 184 64 GCTCTGGAGTCAAGTACACCAAGTCGGACTTACGGTTAATTGAAGTCACTGAGACCATTT CGAGGGAGGAAGCGCCGCCGGGTCCGCTCTGCTCTGGGTCCGGCTGGGCCATGGAGTCCA 347 recereadecececerececreterrerecriterrecerrecretecrecrecere GATTGCCCCAGCAAATGCGAAGTGTGCAAGTATGTTGCTGTGGAGCTGAAGTCGGCTTTTG GCCTGCCCAGCAAATGCGAAGTGTGTAAATATGTTGCTGTGGAGCTGAAGTCAGCCTTTG AGGAAACGGGAAAGACCAAGGAAGTGATTGACACCGGCTATGGCATCCTGGACGGAAGG CCTCTGGAGTCAAATACACCCAAGTCGGACTTGCGGTTAATCGAAGTCACTGAGACCATTT GCAAGAGGCTTCTGGACTACAGCCTGCAAGGAGGACTGGCAGCAACAGGATTTGCCA AGGGTATGTCGGAGACCTTTGAGACGCTGCACAACCTAGTCCACAAAGGGGGTCAAGGTGG AGGGCATGTCAGAGACCTTTGAGACATTACACAACCTGGTACACAAAGGGGTCAAGGTGG 245 527 305 587 365 647 425 707 485 125 407 185 467 65 g ద 8 6 ò g 8 ò ð 셤 ò 셤 ò 셤 ð

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The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polynucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, a method for stimulating the problemation of chondrocyte cells and a method for correcting the presence of a tumour in a mammal (e.g. lung, colon, breast, prostate, rectal, cervical and liver tumours). The polynucleotides are consected in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating suese as hybridisation probes, in chromosome and gene mapping, in generating suesting PRO colon, propertides by recombinant techniques and in generating either transgenic animals or knock-out animals which are useful in the colophopeptides by recombinant techniques and in generating enter for transgenic animals or knock-out animals which are useful in the development and screening of therapeutically useful reagents. The PRO polypeptides or antibodies are used in preparing a medicament for creating a condition responsive to the polypeptides or antibodies are used in preparing an edicament for as tumours, for modulating the uptake of glucose or FPA by adipocyte cells, for stimulating the proliferation of inner ear urricular cartilage, for stimulating the proliferation of cyproceoglycans from pericyte cells, for stimulating the release of proteoglycans from pericyte cells, for stimulating the release of cycchines from PROC cells, for inhibiting the binding of A-peptide to factor VIIA, for inhibiting the differentiation of adipocyte cells and for stimulating the proliferation of supporting a human PRO proliferation of endothelial cells. This sequence represents a human PRO polymucleotide of the invention. Note: The sequence data for this patent consideration colon sequence. The sequence data for this patent consideration colon sequence.
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/ AL, Sherwood S;
Wood WI, Zhang Z;
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Pred. No. 7e-168;
0; Mismatches 139; Indels 6;
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A, Godowski PJ, Gurney A
Tumas D, Watanabe CK, Wo
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                                    2001WO-US020116
2001WO-US020106
2001WO-US021735.
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2001US-00921836.
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2001US-00887879
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Gerritsen ME, Goddard A,
Smith V, Stewart TA, Tum
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Matches 791; Conservative
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21-JUN-2001; 2
22-JUN-2001; 2
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                protein.
PRO4409.
Human; secreted and transmembrane protein; PRO; gene; ss;
Tumour necrosis factor alpha release; TNF-alpha release;
Jucose uptake modulator;
cell proliferation stimulator; cell differentiation stimulator;
cell differentiation inhibitor; cytokine release stimulator; tumour;
lung tumoue; colon tumour; breast tumour; prostate tumour; rectal tumour;
cervical tumour; liver tumour; chromosome mapping; gene mapping;
gene therapy; chromosome identification; chromosome marker.
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                                                             CCCCTGGAGTCAAATACACCAAGTCGGACTTCCGGTTAATCGAAGTCACAGAGACCATTT 646
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GCCTGCCCAGCAAATGCGAAGTGTGTAAATATGTTGCTGTGGAGCTGAAGTCAGCCTTTG 526
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The invention describes 305 nucleic acids encoding PRO (secreted and transmembrane) polypeptides (I). (I) is useful for stimulating the release of TNF-alpha from human blood, for modulating the uptake of glucose or FFA by skeletal muscle cells or adipocyte cells, for stimulating the proliferation or differentiation of chondrocyte cells, for stimulating the proliferation of or gene expression in pericyte cells, for stimulating the proliferation of inner ear utricular supporting cells, for stimulating the proliferation of T-lymphocyte cells, for stimulating the proliferation of T-lymphocyte cells, for stimulating the proliferation of T-lymphocyte cells, for stimulating cells, for stimulating proliferation of endothelial cells, for stimulating proliferation of endothelial cells, for detecting the presence of tumour in a mammal. The tumour is lung, colon, breast, the presence of tumour in a mammal. The tumour is lung, colon, breast, prostate, rectal, cervical or liver tumour is lung, colon, breast, constants probes are useful for isolating genomic and cDNA nucleotide sequences or antisense probes. (I) is also useful as therapeutic agent. PRO is useful in theraction. A polynucleotide (II) encoding (I) is useful in chromosome and gene mapping, in generation of antisense RNA and DNA, in the preparation of PRO polypeptide, for generating transgenic animals or received to the preparation of subserving transgenic animals or received to the preparation of propertice for generating transgenic animals or received to the preparation of propertice for generating transgenic animals or received to the preparation of propertice for generating transgenic animals or received to the preparation of animals or received to the propertice for the preparation of subserving the propertice or the propertice for generating transgenic animals or received to the propertice for generating transgenic animals or received to the propertice for the propertice for generating transgenic animals or received to the propertice or the propertice for ge
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A, Godowski PJ, Gurney AL, Sherwood S;
Tumas D, Watanabe CK, Wood WI, Zhang Z;
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Gerritsen ME, Goddard A,
Smith V, Stewart TA, Tum
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20-DEC-2000;
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244 304 | TGCAGAAGGCATCGCCCTCCCACAGCCCCCCTGATGAGCTGTGAGCCCAGCTTAGTG 898 typing. This sequence encodes 124 406 TCCTTCCTGCCCCGAAGCTAGGCCCCGAGTCCCGCCGGGGCTGAGGAGACCGACTGGGTGC 184 466 526 586 364 646 424 706 484 766 544 826 604 886 664 724 778 838 64 knockout animals which in turn are useful in the development and screening of therapeutically useful reagents, in gene therapy, for chromosome identification, as chromosome marker, and for generating probes. An anti-(1)-antibody is useful in diagnostic assays for PRO, edetecting its expression in specific calls, tissues or serum, and for affinity purification of PRO from recombinant cell culture or natural sources. (I) and (II) are useful for tissue typing. This sequence enco GATTGCCCAGCAAATGCGAAGTGTGCAAGTATGTTGCTGTGGAGCTGAAGTCGGCTTTTG AGGAAACGGGAAAGACCAAGGAAGTGATTGACACCGGCTATGGCATCCTGGACGGAAGG GCAAGAGGCTCCTGGATTATAGCCTGCACAAGGAGGAGGACGGCAGCAATCGATTTGCCA CGAGTTGCCTAGCAGAGCGGTGGTCTGGCAAGAAGGGGGGACATAGCCTCCCTGGGAGGAA 1007 AGAAGTCCAAGAAGAAGAGAGGAGGCCAAGGCAGCAGCGGCAGGAGTAGCAGCAGCA GCTCTGGAGTCAAGTACACCAAGTCGGACTTACGGTTAATTGAAGTCACTGAGACCATTT 587 CCTCTGGAGTCAAATACACCCAAGTCGGACTTGCGGTTAATCGAAGTCACTGAGACCATTT GCAAGAGGCTTCTGGACTACAGCCTGCACAAGGAGGACTGGCAGCAACCGGTTTGCCA AGGGTATGTCGGAGACCTTTTGAGACGCTGCACAACCTAGTCCACAAAGGGGTCAAGGTGG AGGCATGTCAGAGACCTTTGAGACATTACACAACCTGGTACAAAAGGGGTCAAGGTGG 767 TGATGGACATCCCCTATGAGCTGTGGAACGAGACTTCTGCAGAGGTGGCTGACCTCAAGA AGCAGTGTGACGTGCTGGTGGAAGAGTTTGAAGAGGTGATTGAGGACTGGTACAGGAACC 827 AGCAGTGTGTGTGCTGGTGGAAGAGTTTGAGGAGGTGATCGAGGACTGGTACAGGAACC ACCAGGAGGAAGACCTGACTGAATTCCTCTGTGCCAACCACGTGCTGAAGGGAAAGGACA ccaerreccrescaeaecaerecrescaasaaeaecaecaecaecreccereseaeae 725 AGAAATCCAAGAAGAAGCGCAGCGGAGTCAAG-----GGCTCCTCCAGTGGCAGCAGCA 779 AGCAGAGGAAGGAACTGGGGGCCTGGGGGAGGATGCCAACGCCGAGGAGGAGGAGGAGGTG CGAGGGAGGAAGCGCCGCCGGGTCCGCTCTGGGTCCGGCTGGGCCATGGAGTCCA TGATGGATATCCCCTATGAGCTGTGGAACGAGACCTCAGCAGAGGTGGCTGACCTCAAGA Gaps . 9 Score 691.6; DB 9; Length 1675; Pred. No. 7e-168; Sequence 1675 BP; 380 A; 469 C; 520 G; 306 T; 0 U; 0 Other; a novel human secreted and transmembrane PRO polypeptide 0; Mismatches 139; Indels 37.6%; 84.5%; Best Local Similarity 84.5 Matches 791; Conservative 467 245 305 647 707 545 947 1067 S 287 125 185 527 365 425 605 665 839 485 Query Match 8888888888888 셤 a 셤 셤 유 ద 셤 요 g 셤 유 용 ઠ ò ઠે ò δ ઠે ઠ 셤 ò ਨੇ ठ ⋧ ò · & ò 요

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Novel secreted and transmembrane PRO polypeptides useful for stimulating the release of tumor necrosis factor alpha and detecting the presence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; Fig 135; 660pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                the release of tumor
a tumor in a mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; ADB19144.
Human; secreted and transmembrane protein; PRO; gene; ss;
Tumour necrosis factor alpha release; TNF-alpha release;
glucose uptake modulator;
cell proliferation stimulator; cell differentiation stimulator;
cell differentiation inihibitor; cytokin.
                                                                                                   Novel human secreted and transmembrane protein PRO4409 cDNA
                     1187 CCTCTGTGAGACCCCTGATTTTGAAGCTGAGGA 1222
             899 TCCTTGAATCAAGACCCCTGACTTCAGAGCTTGGGA 934
                                                           ADB19143 standard; cDNA; 1675 BP
                                                                                                                                                                                                                                                                                                       98WO-US025108.
99WO-US000106.
99WO-US005190.
99WO-US00615.
99WO-US010733.
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98WO-US019093.
98WO-US019094.
98WO-US019177.
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98WO-US024855.
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99WO-US031274.
2000WO-US000219.
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98WO-US019437
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30-DEC-1999;
05-JAN-2000;
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29-OCT-1998;
20-NOV-1998;
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05-JAN-1999;
08-MAR-1999;
10-MAR-1999;
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15-SEP-1999
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Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, G
Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
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2001US-00802706.
2001US-00802899.
2001US-00812844.
2001US-00854208.
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2001US-00874503.
2001US-00882636.
2001US-00886342.
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2000WO-US030952.
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2001US-00796498.
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2001US-00924419.
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2000WO-US007377
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23-AUG-2000;
08-NOV-2000;
10-NOV-2000;
10-DEC-2000;
20-DEC-2000;
28-FEB-2001;
28-FEB-2001;
01-MAR-2001;
01-MAR-2001;
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29-JUN-2001;
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24-FEB-2000;
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Gao W;

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1187 CCTCTGTCCTGAGACCCCTGATTTTGAAGCTGAGGA 1222
                                                  Search completed: December 29, 2005, Job time: 1059 secs
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                                                                                                                                                              Gaps
The invention describes 305 nucleic acids encoding PRO (secreted and transmembrane) polypeptides (I). (I) is useful for stimulating the release of TNF-alpha from human blood, for modulating the uptake of glucose or FPA by skeletal muscle cells or adiporyt
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                                                                                                                       Query Match 37.6%; Score 691.6; DB 9; Length 1675; Best Local Similarity 84.5%; Pred. No. 7e-168; Matches 791; Conservative 0; Mismatches 139; Indels 6;
                                                                                       Sequence 1675 BP; 380 A; 469 C; 520 G; 306 T; 0 U; 0 Other;
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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IMMEDIATE SOURCE:
LIBRARY: THPINOB01
CLONE: 030137
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                                                                                                                                                 Sequence 14, Appl
Sequence 14, Appl
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Sequence 2, Appl
Sequence 17521, A
Sequence 17521, A
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Sequence 20, Appl
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Sequence 91307, A
Sequence 16775, A
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Sequence 1, Appli
                                                                                                                                                                      December 29, 2005, 22:40:35; Search time 355 Seconds (without alignments) 9208.270 Million cell updates/sec
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1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*

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3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

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                     GenCore version 5.1.6
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US-09-163-285-3
US-09-163-285-3
US-09-163-285-1
US-09-949-016-14364
US-09-949-016-14364
US-09-249-016-14364
US-09-130-114-2
US-09-130-114-2
US-09-949-016-17521
US-09-949-016-17521
US-09-130-114-2
US-09-130-114-2
US-09-130-11-17521
US-09-10-17521
US-09-10-399-1
US-09-10-399-1
US-09-1757-669A-20
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US-09-949-016-13584
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                         - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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seq length: 200000000
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1839
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Match Length
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Sequence 14581, A
Sequence 12147, A
Sequence 17361, A
Sequence 1343, A
Sequence 1803, A
Sequence 2, Appli
Sequence 1, Appli
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APPLICANT: Cocke, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE J.508
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                          ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
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RILING DATE:
CLASSIPICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REPERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 845-055
TELEFEXX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 140:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 1201 base pairs
"""". nucleic acid
Sequence 140, Application US/09023655; Patent No. 6607879; GENERAL INFORMATION:
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Sequence 13584,

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PALO ALTO
CALIFORNIA
                                  USA
                                              94304
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US-09-023-655-274
                               COUNTRY:
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Sequence 274, Application US/09023655
Patent No. 6607879
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Geffrey J. Sellhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAGGTGGCTGACCTCAAGAAGCAGTGTGATGTGCTGGTGGAAGAGTTTGAGAAGAAGCATC
                                                                                             228 GCTGAAGTCGGCTTTTGAGGAAACGGGAAAGACCAAGGAAGTGATTGACACCGGCTATGG
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                                 Length 1201;
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                                 25.4%; Score 467; DB 3; I
79.0%; Pred. No. 4.1e-109;
iive 0; Mismatches 95;
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                                               Best Local Similarity
Matches 612; Conser
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US-09-023-655-274
    US-09-023-655-140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
SOFTWARE: Word Perfect
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION:
APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 458.6; DB 3;
Pred. No. 6.3e-107;
); Mismatches 92;
                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: 94-0001 US
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION SEC 1650 845-4166
INFORMATION FOR SEC 1D NO: 274:
SEQUENCE CHARACTERISTICS:
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84.8%;
                       Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1534 base pairs
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Best Local Similarity 84.8
Matches 525; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LIBRARY: BRSTNOT07
CLONE: 1298861
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GTTAATTGAAGTCACTGAGACCATTTGCAAGAGGCTTCTGGACTACAGGCTGCACAAGGA 398
                                                               255 deriggaagagecerragagaarrrareneaecegareeregacraragrerreaecerea 314
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                                                                                                                                                                                                                                                                                                     519 CTCAGCAGAGGTGGCTGACCTCAAGAAGCAGTGTGACGTGCTGGTGGAAGAAGAGTTTGAAGA
                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Khodadoust, Mehran
TITLE OF INVENTION: NOVEL MSP-5 PROTEIN AND NUCLEIC ACID MOLECULES
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RPPLICATION NUMBER: US/09/163,285
FILING DATE:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: June 24, 1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: M
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Mandragouras, Amy E. REGISTRATION NUMBER: 36,20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (617) 227-7400
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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CITY: Boston
STATE: Massachusetts
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                                                                        200 GAAGCAGTGTGTGTGCTGGTGGAGGTTTGAGGGGGGTGATCGAGGACTGGTACAGGAA 1259
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                                                543 GAAGCAGTGTGACGTGCTGGTGGAAGAGTTTGAAGAGGTGATTGAGGACTGGTACAGGAA
                                                                                                                                                                                                                                                                                            Sequence 3, Application US/09163285
Patent No. 6204013
GENERAL INFORMATION:
APPLICANT: KNodadoust, Mehran
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/163,285
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Pred. No. 6.9e-31;
0; Mismatches 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                       60/090,398
                                                                                                                                          603 CCACCAGGAGGAAGACCTG 621
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PRIOR APPLICATION DATA:
APPLICATION UNDER: 60/090,39-
FILING DATE: June 24, 1998
ATTORNEY/AGENT INFORMATION:
NAWE: MANDERGUARS, AMY E.
REGISTRATION NUMBER: 36,207
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 8.7%;
Best Local Similarity 57.3%;
Matches 310; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 28 State Str
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
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US-09-163-285-3
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US-09-482-273-23
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                                                                                                                                                         Similarity 57.3%; Score 160.2; DB 3; Length Similarity 57.3%; Pred. No. 9e-31; Conservative 0; Mismatches 228; Indels
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APPLICANT: Rosen et al.
TITLE OF INVENTION: 71 Human Secreted Proteins
FILE REFERENCE: 22030P1
CURRENT APPLICATION NUMBER: US/09/482,273
CURRENT APPLICATION NUMBER: US/09/482,273
CURRENT FILING DATE: 2000-01-13
EARLIER PILING DATE: 1999-07-14
EARLIER FILING DATE: 1999-07-14
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER APPLICATION NUMBER: 60/092,925
EARLIER APPLICATION NUMBER: 60/092,925
EARLIER APPLICATION NUMBER: 60/092,925
EARLIER APPLICATION NUMBER: 60/092,925
EARLIER APPLICATION NUMBER: 60/092,926
EARLIER FILING DATE: 1998-07-15
NUMBER: OF SEQ ID NOS: 267
SOFTWARE: PARENTIN VET. 2.0
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Patent No. 6534631
    CDS
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US-09-482-273-23/c
                                                                                                                                                         Query Match
Best Local Simi
Matches 310;
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LENGTH: 1658
; NAME/KEY:
; LOCATION:
US-09-163-285-1
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                                                                                                                                                                       728 AATCCAAGAAGAGCGCAGCGGAGTCAAG-----GGCTCCTCCAGTGGCAGCAAGC
                                                                                    668 GTTGCCTAGCAGAGCGGTGGTCTGGCAAGAAGGGGGACATAGCCTCCCTGGGAGGAGAA
                                        Gaps
                                          9
Length 1658;
                                          Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
  DB 3;
                                            29;
Score 156.6; DB 3
Pred. No. 7.8e-30;
0; Mismatches 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                   902 TIGAATCAAGACCCCTGACTTCAGAGCTTGGGA 934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68 crerceadacecerdarrirgaadergadda 36
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PILLING DATE: 26-AUG-1991
ATTORNEY AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 39,708
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)83-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
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SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
  8.5%;
                                            Conservative
  Query Match
Best Local Similarity
Matches 208; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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425 AGGGTATGTCGGAGACCTTTGAGACGCTGCACAACCTAGTCCACAAAGGGGTCAAGGTGG
                                                                          485 TGATGGATATCCCCTATGAGCTGTGGAACGAGACCTCAGCAGAGGTGGCTGACCTCAAGA
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3.1%; Score 56.2; DB 2; Length 7
Best Local Similarity 7.2%; Pred. No. 0.00058;
Matches 31; Conservative 222; Mismatches 180; Indels
                                                                                                                                                                                                                                                                                                                                                    APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F.
ALIEL OF INVENTION: RECOMBINANT FOWLFOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMM
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                            ; Sequence 14, Application US/08232463; Patent No. 5670367; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear IMMEDIATE SOURCE: CLONE: pTZgpt-F18
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                                                                                                                                                         545 AGCAG 549
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TELEX: 8
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US-08-232-463-14
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TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: 00/241,755
PRIOR PELLING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER: 60/231,498
NUMBER OF SEQ ID NOS: 207012
SOUTHARD SESEQ FOR Windows Version 4.0
SEQ ID NO 14364
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                                                                                                                                      393 CAAGGAGAGACTGGCAGCAACCGGTTTGCCAAGGGTATGTCGGAGACCTTTGAGACGCT 452
                                                                                                                                                                                                                   GCACAACCTAGTCCACAAAGGGGTCAAGGTGGTGATGGATATCCCCTATGAGCTGTGGAA 512
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                                                     Query Match
4.1%; Score 75.2; DB 2; Length 7218;
Best Local Similarity 7.2%; Pred. No. 8.2e-09;
Matches 32; Conservative 241; Mismatches 169; Indels 0.
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10S-09-949-016-14364/c
; Sequence 14364, Application US/09949016
; Patent No. 6812339
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CCATION: (1)...(24207)
OTHER INFORMATION: n = A,T,C or G
; CLONE: pTZgpt-Fls
US-08-232-463-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Human
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3.0%; Score 55.4; DB 2;
46.5%; Pred. No. 0.00055;
tive 0; Mismatches 206;
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                                                     GAGGAGGAGGAGGTGTGCAGAAGG
                                                                                                         ; Sequence 2, Application US/09130114; Patent No. 5976807; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                            Best Local Similarity 46.5
Matches 179; Conservative
                                                                                                                                                                                                                                                                                   ORGANISM: EBNA
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US-09-949-016-5779
                                                                                                 US-09-130-114-2/c
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                                                                                                                                                         CTCCCACGCCCCCACACACACCATAAAATTATTTCGATGCTGTTTCATAACTGTAAAA 1824
                                                                                                                                                                                                  TCTTTTTGCCTTTGTCCCCCAATCCCAGGGGTGGAAGGCCATCACCATCATTGGAGGC 1644
                                                                     TTTTGGCCTTTTCGGTTTGGTTCCTGGGTCCTCATCAGCCTCCAGAGTGTCCCCTCATCGA 1584
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (1). T(1926)
OTHER INFORMATION: template strand of EBNA-1 DNA
                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Epstein Barr Virus
                                                                                                                                                                                                                                 1825 AAAAAAAAAAA 1837
                                                                                                                                                                                                                                                     1472 ATAGGTAATTACA 1484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORM;
US-09-249-585A-4
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Sequence 5779, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TILE REFERENCE: CL00130,
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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APPLICANT: Horlick, Robert A.
APPLICANT: Damaj, Bassam B.
APPLICANT: Damaj, Bassam B.
APPLICANT: Robbins, Alan K.
TITLE OF INVENTION: Evantavotic Cells Stably Expressing Genes TITLE OF INVENTION: From Multiple Transfected Episomes FILE REFERENCE: 0867/1D903US1
CURRENT APPLICATION NUMBER: US/09/130,114
CURRENT FILING DATE: 1998-08-06
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FASTSEQ for Windows Version 3.0
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New York
          Best Local Similarity
Matches 181; Conserv
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US-08-728-323A-1
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GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: 06/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PRIESEQ FOR WINDOWS VERSION 4.0

LENGTH: 87734
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PRIOR APPLICATION NUMBER. 60/237,768
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FREUSE FOR Windows Version 4.0
SEQ ID NO 5779
LENGTH: 3130
TYPE: DNA
ORGANISM: Human
US-09-949-016-5779
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Patent No. 6812339
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181; Conserv
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US-09-949-016-17521
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Best Local S
Matches 181
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2.7%; Score 49.4; DB 3; Length 87734;

Query Match

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60363 CCACCAGCAGAACATGGGCTAATGGACAACTGGAATCCAAGCTGGACTCGCTGGCTT
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Patent No. 5948676

GENERALI INFORMATION:

APPLICANT: Changy Yuan

APPLICANT: Changy Yuan

APPLICANT: Behenzky, Roy A.

APPLICANT: Behenzky, Roy A.

APPLICANT: Behenz, Isidore S.

APPLICANT: Moore, Patrick S.

TITLE OF INVENTION: Immediate Early Protein From Kaposi's

TITLE OF INVENTION: Brocoma Associated Herpesvirus, DNA

TITLE OF INVENTION: Encoding Same And Uses Thereof

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooper & Dunham LLP
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728,323A
ilarity 47.3%; Pred. No. 0.082;
Conservative 0; Mismatches 201;
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STREET: 1185 Avenue of the Americas
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ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575,
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      I: Floppy disk
IBM PC compatible
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MEDIUM TYPE: Floppy
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745

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2481 GCAGGAGCAGGAGTTAGAGGAGCAGGAGCAGGAGTTAGAGGAGCAGGAGCACGTGCAAGAGCA 2540
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Pred. No. 0.038;
0; Mismatches 204;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09410399; Batent No. 648287; GENERAL INFORMATION:
APPLICANT: Robertson, Erle S.
TITLE OF INVENTION: Methods to Inhibit or E; TITLE OF INVENTION: to Genomic Host DNA; TITLE OF INVENTION: to Genomic Host DNA; CURRENT APPLICATION NUMBER: US/09/410,399; CURRENT FILING DATE: 1999-10-01
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Matches 194; Conservative
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US-09-410-399-1
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US-09-410-399-1
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SEQ ID NO 1
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APPLICANT: Kieff, Elliott D.
APPLICANT: Kieff, Elliott D.
APPLICANT: Asye, Kenneth M.
APPLICANT: Asye, Kenneth M.
TITLE OF INVENTION: RHADINO VIRUS LANA ACTS IN TRANS ON A UNIT OF RHADINO TITLE OF INVENTION: VIRUS DNA TO MEDIATE EFFICIENT EPISOME PERSISTENCE FILE REFERENCE: 16412-10001R
CURRENT APPLICATION NUMBER: US 60/109,422
EARLIER APPLICATION NUMBER: US 60/109,422
EARLIER PILING DATE: 1999-04-21
EARLIER PILING DATE: 1999-11-19
SOGTWARE: PALENTIN Ver. 2.0
SEQ ID NO 3.
                                                                                                                                                                                                                                                          446 AGACGCTGCACAACCTAGTCCACAAAGGGGTCAAGGTGGTGATGGATATCCCCTATGAGC
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Pred. No. 0.038;
0; Mismatches 204; Indels 3.
                                                                                                                                                                      Score 48.6; DB 2; Length 3489;
Pred. No. 0.038;
0; Mismatches 204; Indels 3
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; ORGANISM: Kaposi's sarcoma-associated herpesvirus
(18-09-298-568-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
US-09-298-568-1
Sequence 1, Application US/09298568
Patent No. 6322792
GENERAL INFORMATION:
                                               MOLECULE TYPE: DNA (genomic)
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Best Local Similarity 48.4%;
Matches 194; Conservative
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Best Local Similarity 48.4
Matches 194; Conservative
        single
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COCATION:
US-08-728-323A-1
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(cgn2_6/ptodata/1/pubpna/USO9B_PUBCOMB.seq: *

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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd
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US-10-123-904-135
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US-10-140-470-135
US-10-176-918-135
US-10-176-918-135
US-10-176-918-135
US-10-142-431-135
US-10-142-419-135
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US-10-123-261-135
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Maximum Match 100%
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App	App	App	App	App	App	App	App	App	App	App	App										
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Seguence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Seguence	Sequence						
US-10-140-921-135	US-10-140-928-135	US-10-121-045-135	US-10-123-292-135	US-10-123-903-135	US-10-124-819-135	US-10-124-822-135	US-10-140-925-135	US-10-160-498-135	US-10-124-824-135	US-10-127-825A-135	US-10-127-829A-135	US-10-127-835A-135	US-10-127-839A-135	US-10-127-901A-135	US-10-128-693A-135	US-10-131-813A-135	US-10-131-818A-135	US-10-131-823A-135	US-10-131-824A-135	US-10-131-830A-135	US-10-131-837A-135
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ALIGNMENTS

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APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLECTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-KB PATHW)
FILE REPERENCE: D0108.np
CURRENT APPLICATION NUMBER: US/10/126,103
CURRENT FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: US 60/284,962
PRIOR PLING DATE: 2001-04-19
PRIOR PLING DATE: 2001-04-19
PRIOR PLING DATE: 2001-04-26
PRIOR PELICATION NUMBER: US 60/286,645
PRIOR PLING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 284
SOFTWARE: PATENTIN VERSION 3.0
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Pred. No. 6.6e-197;
0; Mismatches 139;
                                       Sequence 139, Application US/10126103 Publication No. US20030224486A1 GENERAL INFORMATION:
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Best Local Similarity 84.5%;
Matches 791; Conservative C
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US-10-126-103-139
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Sequence

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US-10-028-072-135
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TITLE OF INVENTION: POLYNUCLECTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-KB

TITLE OF INVENTION: PATHWAY

TITLE OF INVENTION: PATHWAY

TITLE OF INVENTION: PATHWAY

TITLE OF INVENTION: PATHWAY

CURRENT APPLICATION NUMBER: US /10/431,096

CURRENT FILING DATE: 2003-08-07

PRIOR PILING DATE: 2001-04-19

PRIOR PILING DATE: 2002-04-19

PRIOR PAPLICATION NUMBER: US 60/286,645

PRIOR PAPLICATION NUMBER: US 60/286,645

PRIOR APPLICATION NUMBER: US 60/346,986

PRIOR PILING DATE: 2001-04-26

PRIOR PILING DATE: 2001-04-26

PRIOR APPLICATION NUMBER: US 60/346,986

PRIOR PILING DATE: 2002-01-09

NUMBER OF SEQ ID NOS: 307

SEQ ID NO 139

LENGTH: 1378
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                   GCTCTGGAGTCAAGTACACCAAGTCGGACTTACGGTTAATTGAAGTCACTGAGACCATTT
                                CCTCTGGAGTCAAATACACCAAGTCGGACTTGCGGTTAATCGAAGTCACTGAGACCATTT
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Publication No. US20040086896A1
GENERAL INFORMATION:
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CRGANISM: Homo
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US-10-431-096-139
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 DB 7;
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Score 691.6; DB 7;
Pred. No. 6.6e-197;
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37.6%;
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Query Match 37.6
Best Local Similarity 84.5
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PRIOR FILING DATE: 1998-01-23
PRIOR FILING DATE: 1998-01-23
PRIOR FILING DATE: 1998-01-23
PRIOR FILING DATE: 1998-02-04
PRIOR FILING DATE: 1998-02-04
PRIOR PLICATION NUMBER: 60/074086
PRIOR APPLICATION NUMBER: 60/074092
PRIOR APPLICATION NUMBER: 60/074092
PRIOR PILING DATE: 1998-02-09
PRIOR FILING DATE: 1998-03-12
PRIOR FILING DATE: 1998-03-12
PRIOR FILING DATE: 1998-03-20
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PRIOR APPLICATION NUMBER: 60/081818
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PRIOR APPLICATION NUMBER: 60/08299
PRIOR PILING DATE: 1998-04-24
PRIOR FILING DATE: 1998-04-24
PRIOR APPLICATION NUMBER: 60/08332
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PRIOR PILING DATE: 1998-04-29
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PRIOR APPLICATION NUMBER: 60/066770
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R APPLICATION NUMBER: 60/084627
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FILING DATE: 1998-04-09
APPLICATION NUMBER: 60/081695
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APPLICATION NUMBER: 60/064809
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FILING DATE: 1997-11-12
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APPLICATION NUMBER: 60/066511
TITLE DATE: 1997-11-24
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APPLICATION NUMBER: 60/081203
FILING DATE: 1998-04-09
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APPLICATION NUMBER: 60/081817
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APPLICATION NUMBER: 60/064248
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FILING DATE: 1997-11-17
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FILING DATE: 1997-12-16
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APPLICATION NUMBER: 60/066364
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TITLE OF INVANTION:
FILE REFERENCE:
CURRENT FILING DATE: 2001-12-19
PRIOR PELING DATE: 1997-06-18
PRIOR PELING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-19
PRIOR PELING DATE: 1997-10-17
PRIOR PELING DATE: 1997-10-17
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APPLICATION NUMBER: 60/063733
FILING DATE: 1997-10-29
Publication No. US20030004311A1
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Watanabe, Colin K
Wood, William
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Gerritsen, Mary E
Goddard, Audrey
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                                                   Baker, Kevin P.
Beresini, Maureen
DeForge, Laura
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Filvaroff, Ellen
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APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
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APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Filvaroff, Ellen
APPLICANT: Geo, Wei-Qiang
APPLICANT: Geo, Wei-Qiang
APPLICANT: Gedard, Audrey
APPLICANT: Godoard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Sherwood, Steven
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
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Pred. No. 7.1e-197;
0; Mismatches 139;
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R FILING DATE: 1998-06-07

R APPLICATION NUMBER: 60/088730

R FILING DATE: 1998-06-10

R FILING DATE: 1998-06-10

R FILING DATE: 1998-06-10

R APPLICATION NUMBER: 60/08810

R RILING DATE: 1998-06-10

R APPLICATION NUMBER: 60/08858

R FILING DATE: 1998-06-17

R APPLICATION NUMBER: 60/08959

R FILING DATE: 1998-06-17

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              R APPLICATION NUMBER: 60/085323
R FILING DATE: 1998-05-13
R APPLICATION NUMBER: 60/085338
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R APPLICATION NUMBER: 60/085339
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FILING DATE: 1998-06-23
APPLICATION NUMBER: 60/090429
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APPLICATION NUMBER: 60/090445
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APPLICATION NUMBER: 60/087106
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APPLICATION NUMBER: 60/088026
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Pred. No. 7.1e-197;
0; Mismatches 139;
TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P333OR.C182
CURRENT APPLICATION NUMBER: 20/10/140,808
CURRENT FILING DATE: 2002-05-07
Prior Apploication removed - See File Wrapper or NUMBER OF SEQ ID NOS: 550
LENGTH: 1675
                                                                                                                                                              Query Match 37.6%;
Best Local Similarity 84.5%;
Matches 791; Conservative
                                                                                                                        ORGANISM: Homo Sapien
US-10-140-808-135
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C17
CURRENT APPLICATION NUMBER: US/10/121,049
CURRENT FILING DATE: 2002-04-12
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llarity 84.5%; Pred. No. 7.1e-197;
Conservative 0; Mismatches 139;
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                                                         TCCTTGAATCAAGACCCCTGACTTCAGAGCTTGGGA
                                                                                                                                                                               ; Sequence 115, Application US/10121049; Publication No. US20030022239A1; GENERAL INFORMATION:
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Stewart, Timothy A.
Tumas, Daniel
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Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
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Filvaroff, Ellen
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Gerritsen, Mary
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US-10-121-049-135
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Best Local Simi:
Matches 791;
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US-10-121-049-135
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LENGTH: 167
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RESULT 7
US-10-140-470-135
; Sequence 135, Application US/10140470
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APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gartiteen, Mary E.
APPLICANT: Godard, Austin L.
APPLICANT: Godowski, Paul J.
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Tumas, Daniel
APPLICANT: Smith, Victoria
APPLICANT: APPLICANTON: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: NUMBER: US/10/123, 904
CURRENT FILING DATE: 2002-04-16
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Publication No. US20030022328A1
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; ORGANISM: Homo Sapien
US-10-123-904-135
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US-10-123-904-135
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Pred. No. 7.1e-197;
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Conservative
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Best Local Similarity
Matches 791; Conserv
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84.5%; Pred. No. 7.1e-197;
iive 0; Mismatches 139; Indels 6;
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Sequence 135, Application US/10175746
Publication No. US20030027270A1
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Gerritsen, Mary E.
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Filvaroff, Ellen
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Gurney, Austin L.
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Smith, Victoria
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Matches 791, Conservative
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APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tunash, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Wood, William
APPLICANT: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
CURRENT APPLICATION NUMBER: US/10/140,470
CURRENT APPLICATION DATE: 2002-05-06
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NUMBER OF SEQ ID NOS: 550
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84.5%; Pred. No. 7.1e-197;
iive 0; Mismatches 139;
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Filvaroff, Ellen
Gao, Wei-Qiang
Gerritsen, Mary E.
Goddard, Audrey
                                 Baker, Kevin P.
Beresini, Maureen
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Gurney, Austin L.
Sherwood, Steven
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Best Local Similarity 84.5
Matches 791; Conservative
                                                                                               DeForge, Laura
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US-10-140-470-135
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LENGTH: 1675
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Publication No. US20030027275A1
GENERAL INFORMATION:
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APPLICANT: Beresini, Maureen
APPLICANT: Derorge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
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US-10-176-918-135
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APPLICANT: Sherwood, Steven
APPLICANT: Sherwood, Steven
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Abang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C382
CURRENT APPLICATION NUMBER: US/10/176,918
CURRENT FILING DATE: 2002-06-20
CURRENT FILING DATE: 2002-06-20
NUMBER OF SEQ 1D NOS: 550
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                                                                                                                                                                                                                                                                                                                                                                                                                                         37.6%; Score 691.6; DB 5;
84.5%; Pred. No. 7.1e-197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 37.6
Best Local Similarity 84.5
Matches 791; Conservative
                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo Sapien
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484

544

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1067 AACAAAGGAAGGAGCTGGGTGGCCTTGAGGGAGACCCCCAGCCCCGAGGAGGATGAGGGCA 1126
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                                                                          587 CCTCTGGAGTCAAATACACCCAAGTCGGACTTAATCGAAGTCACTGAGACCATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Stewart, Timochy A.
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P3330R1C154
                                                                                                                              GCAAGAGGCTTCTGGACTACAGCCTGCACAAGGAGAGACTGGCAGCAACCGGTTTGCCA
                                                  GCTCTGGAGTCAAGTACACCAAGTCGGACTTAACTTGAAGTCACTGAGACCATTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Desnoyers Lucr
APPLICANT: Filvaroff, Ellen
APPLICANT: Filvaroff, Ellen
APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
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Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
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APPLICANT: Wood, William
APPLICANT: Abod, Milliam
APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT APPLICANT ACTOR ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
CURRENT APPLICATION NUMBER: US/10/176,921
CURRENT APPLICATION ACIDS ENCODING THE SAME
CURRENT APPLICATION NUMBER: US/10/176,921
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                                   1007 AGAAGTCCAAGAAGAAGAGCAGCAGGCCAAGGCAGCAGGGGGGAGTAGCAGCAGCA
                                                                          AGCAGAGGAAGGAACTGGGGGGCCTGGGGGAAGATGCCAACGCCGAGGAGGAGGAGGTG
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NUMBER OF SEQ ID NOS: 550
                                                                                                                                                                                                                                                    CCTCTGTCCTGAGACCCCTGATTTTGAAGCTGAGGA 1222
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Pred. No. 7.1e-197;
0; Mismatches 139;
                                                                                                                                                                                                                                                                                                                                                       Sequence 135, Application US/10176921
Publication No. US20030027276A1
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84.5%;
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Smith, Victoria
Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
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CORGANISM: Homo Sapien
US-10-176-921-135
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LENGTH: 1675
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Best Local 3
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APPLICANT: Watanabb, Colin K
APPLICANT: Watanabb, Colin K
APPLICANT: Wood, William
APPLICANT: Townson, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
CURRENT APPLICATION NUMBER: US/10/140,474
CURRENT FILING DATE: 2002-05-06
Prior Application removed - See Palm or File Wrapper
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1675;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                    1187 CCTCTGTCCTGAGACCCCTGATTTTGAAGCTGAGGA 1222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 691.6; DB 5;
Pred. No. 7.1e-197;
0; Mismatches 139;
             TCCTTGAATCAAGACCCCTGACTTCAGAGCTTGGGA
                                                                                                          ; Sequence 135, Application US/10140474; Publication No. US20030032156A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                   Sherwood, Steven
Smith, Victoria
Stewart, Timothy A.
Tumas, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity 84.5%;
Matches 791; Conservative 0
                                                                                                                                                                                                Desnoyers, Luc
Filvaroff, Ellen
Gao, Wei-Oiang
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
                                                                                                                                                    APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo Sapien
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US-10-140-474-135
                                                                                                US-10-140-474-135
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            CURRENT FILING DATE: 2002-05-03
Prior Application removed - See Palm or File Wrapper NUMBER OF SEQ ID NOS: 550
SEQ ID NO 1135
LENGTH: 1675
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CURRENT APPLICATION NUMBER: US/10/137,865
                                                                                 TYPE: DNA
CORGANISM: Homo Sapien
US-10-137-865-135
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APPLICANT: Beresini, Mauren
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Garitken, Mary E.
APPLICANT: Godwski, Paul J.
APPLICANT: Godwski, Paul J.
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Scewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
APPLICANT: Watanabe, Colin K
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 135
LENGTH: 1675
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ORGANISM: Homo Sapien
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Mismatches 139;
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US-10-143-114-135
Sequence 135, Application US/10143114
Publication No. US20030036180A1
GENERAL INFORMATION:
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C244
CURRENT APPLICATION NUMBER: U5/10/142,419
CURRENT APPLICATION NUMBER: U5/10/142,419
Prior Apploication removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
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Pred. No. 7.1e-197;
0; Mismatches 139;
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; Sequence 135, Application US/10142419
; Publication No. US20030044945A1
; GENERAL INFORMATION:
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Best Local Similarity 84.5%;
Matches 791; Conservative (
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APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Rilen
APPLICANT: Gao, Wei-Oiang
APPLICANT: Gao, Wei-Oiang
APPLICANT: Garitisen, Mary E.
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Filvaroff, Ellen
Gao, Wei-Qiang
Gerritsen, Mary E.
Goddard, Audrey
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Wood, William
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Smith, Victoria
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ORGANISM: Homo Sapien
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APPLICANT: Sherwood, Steven

APPLICANT: Stevent, Timothy A.

APPLICANT: Stevent, Timothy A.

APPLICANT: Stevent, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K

APPLICANT: Wood, William

APPLICANT: Wood, William

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

TITLE OF INVENTION: ACIDS ENCODING THE SAME

FILE REFERRENCE: P3330R1C211

CURRENT APPLICATION NUMBER: US/10/143,114

CURRENT FILING DATE: 2002-05-09

Prior Application removed - See Palm or File Wrapper

NUMBER OF SEQ ID NOS: 550

SEQ ID NO 135
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84.5%; Pred. No. 7.1e-197;
live 0; Mismatches 139;
                                                                         Gao, Wei-Qiang
Gerritsen, Mary E.
 Beresini, Maureen
DeForge, Laura
                                                                                                            Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
                                    Desnoyers, Luc
Filvaroff, Ellen
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Matches 791; Conservative
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ORGANISM: Homo Sapien
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CTCTGGAGTCAATACACCAAGTCGGACTTGCGGTTAATCGAAGTCACTGAGACCATTT 646
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Sequence 10, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 46147, A
Sequence 46147, A
Sequence 11, Appl
Sequence 11, Appl
Sequence 181, Appl
Sequence 183, Appl
Sequence 183, Appl
Sequence 183, Appl
Sequence 186, Appl
Sequence 189, Appl
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                                                                                                                                                             ; Search time 931 Seconds
(without alignments)
1035.506 Million cell updates/sec
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Sequence 195, 1
Sequence 197, 1
Sequence 199, 1
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                                                                                                                                                                                                                                                                                                                                         Published Applications NA New:*

1: /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
2: /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*
5: /cgn2_6/ptodata/1/pubpna/USO1_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/USO1_NEW_PUB.seq:*
7: /cgn2_6/ptodata/1/pubpna/USO1_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/USO1_NEW_PUB.seq:*
9: /cgn2_6/ptodata/1/pubpna/USO1_NEW_PUB.seq:*
9: /cgn2_6/ptodata/1/pubpna/USO1_NEW_PUB.seq:*
10: /cgn2_6/ptodata/1/pubpna/USO0_NEW_PUB.seq:*
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-10-750-185-37066
US-11-121-086-5
US-11-121-086-5
US-10-821-234-49
US-10-821-234-10
US-11-121-086-2
US-11-121-086-16
US-11-121-086-16
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US-10-928-446A-181
US-10-928-446A-183
US-10-928-446A-187
US-10-928-446A-189
US-10-928-446A-191
US-10-928-446A-195
US-10-928-446A-195
US-10-928-446A-195
US-10-928-446A-195
US-10-928-446A-195
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                                                                                                                                                                   December 29, 2005, 23:12:51
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Maximum Match 100%
Listing first 45 summaries
                                                                                                          nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                              IDENTITY NUC
Gapop 10.0 , Gapext 1.0
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seq length: 200000000
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5.7 15346
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Perfect score:
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Maximum DB
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ALIGNMENTS

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USS-10-131-826A-135
Sequence 135, Application US/10131826A
Publication No. Dig20050245730A1
GENERAL INFORMATION:
APPLICANT: Bacreinl, Maureen
APPLICANT: Bacreinl, Maureen
APPLICANT: Bacreinl, Maureen
APPLICANT: Gariteen, Mary E
APPLICANT: Gao, Mei-Cieinen
APPLICANT: Gadard, Audrey
APPLICANT: Gao, Mei-Cieinen
APPLICANT: Gao, Mei-Cieinen
APPLICANT: Gariteen, Mary E
APPLICANT: Mary E
APPLICANT: Mary E
APPLICANT: MARS E
APPLICANT: M
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1067 AACAAAGGAAGGAGCTGGCCTTGAGGGAGACCCCCAGCCCCGAGGAGGATGAGGGCA 1126
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                                  - See File Wrapper or PALM
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9
                                                                                                                                                                                                                                                                                              Length 1675;
                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                 37.6%; Score 691.6; DB 6;
84.5%; Pred. No. 7.6e-169;
tive 0; Mismatches 139;
PRIOR FILING DATE: 1997-09-19
Remaining Prior Application data removed
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 135
                                                                                                                                                                                                                                                                                                                                                                  Matches 791; Conservative
                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                           , ORGANISM: HOWOUT US-10-131-826A-135
                                                                                                                                      LENGTH: 1675
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Sequence 5, Application US/11121086

Sequence 5, Application US/11121086

Publication No. US20050266459A1

GENERAL INFORMATION:
APPLICANT: POULSEN, TIM S.

TITLE OF INVENTION: UNCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES

TITLE OF INVENTION UNMERS: US/11/121,086

CURRENT FILING DATE: 2005-05-00

PRIOR FILING DATE: 2004-05-04

NUMBER OF SEQ ID NOS: 107

SOFTWARE: PATENTIN VORS: 107

SEQ ID NO S: 107

SEQ ID NO S: 107

SEQ ID NO S: 107
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                                                                                     Sequence 37066

10S-10-750-185-37066

1 Sequence 37066, Application US/10750185

1 Publication No. US20050260603A1

2 Publication No. US20050260603A1

3 GENERAL INFORMATION:

APPLICANT: MAI GENOMICS, INC.

APPLICANT: RERR, Richard

APPLICANT: ROSENFELD, David

APPLICANT: HOLM, Tom

APPLICANT: HOLM, Tom

APPLICANT: FANTIN, Dennis

TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS

TILE REFERENCE: MAILIOG-2

CURRENT APPLICATION NUMBER: US/10/750,185

CURRENT APPLICATION NUMBER: US 60/437,482

PRIOR FILING DATE: 2002-12-31

NUMBER OF SEQ ID NOS: 64922

SOFTWARE: PatentIN version 3.1

SEQ ID NO 37066

LENGTH: 946
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Best Local Similarity 43.9%; Pred. No. 0.029;
Matches 258; Conservative 0; Mismatches 327; Indels
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                     DB 6;
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Pred. No. 1.9e-17;
0; Mismatches 21
899 TCCTTGAATCAAGACCCCTGACTTCAGAGCTTGGGA
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Best Local Similarity 84.8%;
Matches 117; Conservative
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US-10-750-185-37066
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Stache-Crain, Birgit
APPLICANT: Adammani, Susan
APPLICANT: Andarmani, Susan
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
TITLE OF INVENTION: WHERE: US/10/821,234
CURRENT PILICATION NUMBER: US 60/462,047
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR APPLICATION NUMBER: US 60/462,047
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt_SEQ_genes Version 1.0
SEQ ID NO 49
                                                                                                                                       751 GTCAAGGGCTCCTCCAGTGGCAGCAGCAGCAGGAAGGAACTGGGGGGCCCTGGGGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         703 GACATAGCCTCCCTGGGAGGGAAGAATCCAAGAAGAAGAGCGCAGCGGAGTCAAGGGCTCC
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Sequence 10, Application WS/10821234
Publication No. US20050255114A1
GENERAL INFORMATION:
APPLICANT: Labat, Ivan
APPLICANT: Applicant: Stache-Crain, Birgit
APPLICANT: Andarmani, Susan
APPLICANT: Tom
APPLICANT: Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
                TGTGCCAACCACGTGCTGAAGGAAAGGACACGAGTTGCCTAGCAGAGCGGTGGTCTGGC
                                                                                                          694 AAG----AAGGGGGACATAGCCTCCCTGGGAGGGAAGAAATCCAAGAAGAAGCGCAGCGGA
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Pred. No. 1.4;
0; Mismatches 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 49, Application US/10821234; Publication No. US20050255114A1; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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Matches 108; Conserv
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                                         14592 AĞĞAĞAĞAĞAĞĞAĞĞAĞĞAĞĞAĞĞAĞGAAÇAĞAĞĞAĞĞAĞĞAĞĞAĞĞAĞĞAĞĞAĞ
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                                                                                         323 CCAAGTCGGACTTACGGTTAATTGAAGTCACTGAGACCATTTGCAAGAGGCTTCTGGACT
                                                                                                                                    4652 AACAGGTGCTAGGACACTGTGGGGACGTCCCAGATGCCAGGGGCAGTGGAGACAGGAGA
                                                                                                                                                                                                                                                                           TTGAGACGCTGCACAACCTAGTCCACAAAGGGGTCAAAGGTGGTGATGGATATCCCCTATG
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APPLICANT: POULSEN, KIRSTEN V.

TITLE OF INVENTION: UNCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES FILE REPERENCE: 09138.6000-00000

CURRENT APPLICATION NUMBER: US/11/121,086

CURRENT FILING DATE: 2005-05-04

PRIOR PILING DATE: 2004-05-04

PRIOR FILING DATE: 2004-05-04

NUMBER OF SEQ ID NOS: 107

SOFTWARE: PATENTIN VERSION 3:3

SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 42.6; DB 7; Length 168516;
Pred. No. 1.2;
0; Mismatches 174; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          800 GCCTGGGGGAGGATGCCAACGCCGAGGAGGAGGAGGAGGTGTGCAGAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 3, Application US/11121086; Publication No. US20050266459A1; GENERAL INFORMATION:
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Best Local Similarity 47.59
Matches 160; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-3
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US-11=121-086-3
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us-09-696~686-47.rnpbn

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61122 GCAGGTCAGAAAATGCCACGCGTGCGCACAGAGGATGGAAGGCCAGGACCCGCCGAAG 61181
                                         Sequence 2, Application US/11121086
; Publication No. US20050266459A1
; GRNERAL INFORMATION:
; APPLICANT: POULSEN, TIMS
; TITLE OF INVENTION:
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; TITLE REPERENCE: 09138.6000-000000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; SOFTWARE: PATENT OF SEQ ID NOS: 107
; SOFTWARE: PATENTIN VERSION 3.3
; SOFTWARE: PATENTIN VERSION 3.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        605 ACCAGGAGGAAGACCTGACTGAATTCCTCTGTGCCAACCACGTGCTGAAGGGAAAGGACA
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Pred. No. 9.5;
                                                                                                                                                                                                                      973 GCTGCTGTCCAGCATCAGGTCTCCTCCTTGG
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Selection US/11121086
Publication No. US20050266459A1
GENERAL INFORMATION:
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Best Local Similarity 43.2%;
Matches 185; Conservative
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US-11-121-086-2
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Publication No. US2005026645941
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVERTION:
TITLE OF INVERTION NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
TITLE OF INVERTION NUMBER: US/11/121,086
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT FILING DATE: 2004-05-04
NUMBER OF SEQ ID NOS: 107
SOFTWARE: PATENTIN VERSION 3.3
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Pred. No. 5.7;
0; Mismatches 175; Indels
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Pred. No. 0.98;
0; Mismatches 110; Indels
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CURRENT APPLICATION NUMBER: US/10/821,234
                                    CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
                                                                                                                                                                    NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt_SEQ_genes Version 1.0
SEQ ID NO 10
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Best Local Similarity 47.0%;
Matches 156; Conservative (
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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LENGTH: 175416
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US-11-121-086-43
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Best Local Similarity 60.4%; Pred. No. 5.5;
Matches 61; Conservative 0; Mismatches
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APPLICANT: Berger, Allison
APPLICANT: Guillemette, Tracv L.
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LOCATION: (235)...(1101)
OTHER INFORMATION: mature IGFBP-2
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Publication No. US20050261230A1
GENERAL INFORMATION:
APPLICANT: Werther, George Arthur
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FEATURE:
Over10N: (1416)...(1420)
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LOCATION: (1433)...(1433)
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LOCATION: (118)...(234)
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1051 TGTGG 1047
                                                                                                                                                 222 TGTGG 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   558 GCTGGTGGAAGAGTTTGAAGAGGTGATTGAGGACTGGTACAGGAACCACCACGAGGAAGA 617
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   102 GCTGCTGCTGCTTCCGCTGCTCCTTCCTGCCCCGAAGCTAGGCCCGAGTCCCGCGG 161
APPLICANT: POULSEN, TIM S.

APPLICANT: NIELSEN, KIRSTEN V.

TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES FILE REFERENCE: 09138 6000-00000
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT FILING DATE: 2005-05-04
PRIOR FILING DATE: 2004-05-04
NUMBER OF SEQ ID NOS: 107
SOFTWARE: PATENTIN VERSION 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                  Score 39; DB 7; Length 189539;
Pred. No. 11;
0; Mismatches 150; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: RERR, RICHARD
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: HOLM, Tom
APPLICANT: FANTH, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
2.0%; Score 37; DB 6; Length 1373;
Best Local Similarity 56.0%; Pred. No. 5.5;
Matches 70; Conservative 0; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28961 ĠĠĠĠŦŤĠĠĠAĊŢĠAĠĠĠĠAĊĠĠŦĠĠĠAĠĠĠAĀĠĀĀĠĠ 28999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             798 GGGCCTGGGGGAGGATGCCAACGCCGAGGAGGAGGAGGGGG 836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 46147, Application US/10750185
Publication No. US20050260603A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Bovine 19866881674802
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 46.2%;
Matches 129; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: MMI1100-2
                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-750-185-46147/c
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                                                                                                                                                                                                                                                SEQ ID NO 16
LENGTH: 189539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 46147
                                                                                                                                                                                                                                                                                                                                         US-11-121-086-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ION: (118)...(1104)
INFORMATION: Insulin-like growth factor binding protein
INFORMATION: (IGFBP-2)
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                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Wraight, Christopher John
APPLICANT: Edmondson, Stephanie Ruth
TITLE OP INVENTION: METHOD FOR THE PROPHYLAXIS AND/OR
TITLE OP INVENTION: TREATMENT OF MEDICAL DISORDERS
FILE REFERENCE: AP32556 071838.0125
CURRENT APPLICATION NUMBER: US/11/090,351
CURRENT FILING DATE: 2005-03-24
PRIOR FILING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 20
SOPTWARE: FASTERQ for Windows Version 3.0
SEQ ID NO 1
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NAME/KEY: allele
LOCATION: (925859)
OTHER INFORMATION: the 'n' at position 925859 may be 'c' or 'g'
                                                                                                                                                                                                                                                       LOCATION: (825765)
OTHER INFORMATION: a "c" may be deleted at this position
                                                                                                                                                                                                                                                                                                                     NAME/KEY: allele
LOCATION: (825828)
OTHER INFORMATION: the 'n' at position 825828 may be
INFORMATION: the 'n' at position 825401 may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the 'n' at position 843055 may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: allele
LOCATION: (826546)
OTHER INFORMATION: the 'n' at position 826546 may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            at position 826654 may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  at position 826826 may
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         at position 843118 may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 at position 871027 may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 at position 871168 may
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                                                                                     at position 825428 may
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                                                                                                                                                                               position 825473
                                                                                                                                                                                                                                                                                                                                                                                                                                                            at position 826041
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LOCATION: (871027)
OTHER INFORMATION: the
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OTHER INFORMATION: the
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OTHER INFORMATION: the
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LOCATION: (827008)
OTHER INFORMATION:
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COCATION: (843055)
THER INFORMATION:
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LOCATION: (871168)
OTHER INFORMATION:
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LOCATION: (843118)
OTHER INFORMATION:
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LOCATION: (872678)
OTHER INFORMATION:
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OTHER INFORMATION:
                                                                                                                                       NAME/KEY: allele
LOCATION: (825473)
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (826041)
OTHER INFORMATION:
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LOCATION: (826863)
OTHER INFORMATION:
                                             NAME/KEY: allele
LOCATION: (825428)
OTHER INFORMATION:
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NAME/KEY: allele
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: allele
              APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Monahan, John E.
APPLICANT: Thibodeau, Steephen N.
APPLICANT: Burgart, Lawrences, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: NWETHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION,
TITLE OF INVENTION: THERAPY OF COLON CANCER
TITLE OF INVENTION: THERAPY OF COLON CANCER
FILE REFERENCE: MPMO1-029P2RNM
CURRENT FILING DATE: 2002-01-21
PRIOR FILING DATE: 2002-11-21
PRIOR FILING DATE: 2002-11-21
PRIOR FILING DATE: 2002-11-20
PRIOR FILING DATE: 2002-03-05
PRIOR PRIOR APPLICATION NUMBER: US 60/361,998
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/361,998
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/361,908
PRIOR PRIOR PRESED FOR WINDOWS VERSION 4.0
SSOFTWARE: FastSEQ for Windows Version 4.0
SSOFTWARE: FastSEQ for Windows Version 4.0
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Publication No. US20050277123A1

GENERAL INCORMATION:

APPLICANT: UNIVERSITY OF UTAH RESEARCH FOUNDATION

TITLE OF INVENTION: VARIANTS OF NEDD4L ASSOCIATED WITH HYPERTENSION AND

TITLE OF INVENTION: VARIANTS OF NEDD4L ASSOCIATED WITH HYPERTENSION AND

TITLE OF INVENTION: VARIANTS OF NEDD4L ASSOCIATED WITH HYPERTENSION AND

TITLE OF INVENTION: VARIANTS OF NEDD4L ASSOCIATED WITH HYPERTENSION AND

TITLE OF INVENTION: VARIANTS OF NEDD4L ASSOCIATED WITH HYPERTENSION AND

TITLE OF INVENTION NUMBER: US/10/928,446A

PRIOR APPLICATION NUMBER: 00/359,741

PRIOR FILING DATE: 2002-02-26

NUMBER OF SEQ ID NOS: 202

SOFTWARE: PALENTIN VET. 2.1

SEQ ID NO 1

LENGTH: 1080000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.0%; Score 36.6; DB 7; Length 6691; 58.9%; Pred. No. 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the 'n' at position 825270 may be 'c'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
Kamatkar, Shubhangi
Schlegel, Robert
Monahan, John E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 58.9
Matches 63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (825234)
OTHER INFORMATION: the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
LOCATION: (82)...(3717)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
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LOCATION: (825270)
OTHER INFORMATION:
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NAME/KEY: allele
LOCATION: (825401)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: allele
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TYPE: DNA
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2.0%; Score 36.6; DB 6; Length 1080000;
Best Local Similarity 50.9%; Pred. No. 78;
Matches 87; Conservative 0; Mismatches 84; Indels 0;
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LOCATION: (1073711)

OTHER INFORMATION: the 'n' at position 1073711 may be 'c' or

US-10-928-446A-1
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INFORMATION: "ttaaaa" may be deleted at this position
                                                                                                                                                                                                                                         NAME/KEY: allele
LOCATION: (1007820)..(1007823)
OTHER INFORMATION: "ttct" may be deleted at this position
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: allele
LOCATION: (1047134)
OTHER INFORMATION: the 'n' at position 1047134 may be 'a'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: allele
LQCATION: (1047378)
OTHER INFORMATION: the 'n' at position 1047378 may be 'c'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: allele
COCATION: (1047739)
OTHER INFORMATION: the 'n' at position 1047739 may be 'a'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: allele
LOCATION: (1066392)
OTHER INFORMATION: the 'n' at position 1066392 may be 'a'
                                                                                                                                                                                                                                                                                                                       NAME/KEY: allele
LOCATION: (1018038)
OTHER INFORMATION: the 'n' at position 1018038 may be 'a'
                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: allele
COCATION: (1018704)
OTHER INFORMATION: the 'n' at position 1018704 may be 'c'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: allele
ACCATION: (1026786)
WIHER INFORMATION: the 'n' at position 1026786 may be 'c'
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NAME/KEY: allele
LOCATION: (993220)
JTHER INFORMATION: the 'n' at position 993220 may be 'c'
                                                        FEATURE:
NAME/KEY: allele
LOCATION: (993254)
OTHER INFORMATION: the 'n' at position 993254 may be 'g'
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LOCATION: (1062808)
OTHER INFORMATION: the 'n' at position 1062808 may be
                                                                                                                                                                              LOCATION: (1006462)
OTHER INFORMATION: the 'n' at position 1006462 may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            at position 1047159 may be
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LOCATION: (1050539)
OTHER INFORMATION: the 'n' at position 1050539 may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANME/KEY: allele
ACCATION: (1018718)..(1018720)
THER INFORMATION: "gtt" may be deleted at this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ä
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LOCATION: (1047159)
OTHER INFORMATION: the
                                                                                                                                                           NAME/KEY: allele
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236760 AGTAGCTGGGATTACAGGCACCCACCATGCCTGGCTAATTTTTTGTATTTTTAGTAG 236701
1547 CTGGGTCCTCATCAGCCTCCAGAGTGTCCCCTCATCGATCTTTTTGCCTTTGTCCCCA 1606
                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: UNIVERSITY OF UTAH RESEARCH FOUNDATION
TITLE OF INVENTION: VARIANTS OF NEDD4L ASSOCIATED WITH HYPERTENSION AND
TITLE OF INVENTION: VIRAL BUDDING
FILE REPERENCE: 0274-5785.1US
CURRENT APPLICATION NUMBER: US/10/928,446A
CURRENT FILING DATE: 2004-08-26
RICH REPLICATION NUMBER: 60/359,741
PRIOR PELICATION DATE: 2002-02-26
NUMBER OF SEQ ID NOS: 202
SOFTWARE: PATENTIN Ver. 2.1
                                                                                                    1607 ATCCCAGGGCTGGAAGGCCATCATCATTGGAGGCTTAACCTGTCAGTTACTAGGAG
                                                                                                                                                                                                                                                 236700 AGACTGGGTTTCACCATGTTGGCCAGGCTGGTCTCAAACTCCTGACCTTAG 236650
                                                                                                                                                                                                      FEATURE:
NAME/KEY: allele
LOCATION: (827008)..(827008)
OTHER INFORMATION: the 'n' at position 827008 may be 'a' or 'g'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: full exon 1 range is 826667-827008
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 181, Application US/10928446A Publication No. US20050277123A1 GENERAL INFORMATION:
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LOCATION: (1002118)..(1002284)
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LOCATION: (843242)..(843315)
OTHER INFORMATION: exon
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OTHER INFORMATION: exon
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OTHER INFORMATION: exon
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OTHER INFORMATION: exon
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OTHER INFORMATION: exon
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US-10-928-446A-181/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 181
LENGTH: 1080000
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NAME/KEY: CDS
LOCATION: (1066207)..(1066314)
OTHER INFORMATION: exon
              FEATURE:
NAME/KEY: CDS
LOCATION: (1006117)..(1006249)
OTHER INFORMATION: excn
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NAME/KEX: CDS
LOCATION: (1018800)..(1018919)
OTHER INFORMATION: exon
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LOCATION: (1026659)..(1026736)
JTHER INFORMATION: exon
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NAME/KEY: CDS
LOCATION: (1047519)..(1047589)
OTHER INFORMATION: exon
                                                                                                                                                                                             LOCATION: (1010940)..(1011014)
OTHER INFORMATION: exon
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INFORMATION: exon
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OTHER INFORMATION: exon
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NAME/KEX: CDS
LOCATION: (1060368)..(1060441)
OTHER INFORMATION: exon
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LOCATION: (1064561)..(1064620)
OTHER INFORMATION: exon
                                                                                                                     LOCATION: (1007860)..(1008036)
OTHER INFORMATION: exon
                                                                                                                                                                                                                                                                LOCATION: (1018160)..(1018291)
OTHER INFORMATION: exon
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OTHER INFORMATION: exon
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OTHER INFORMATION: exon
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THER INFORMATION: exon
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OTHER INFORMATION: exon
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OTHER INFORMATION: exon
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NAME/KEY: CDS
LOCATION: (101
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NAME/KEY: CDS
LOCATION: (104
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NAME/KEY: CDS
LOCATION: (105)
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NAME/KEY: CDS
LOCATION: (100
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NAME/KEY: CDS
LOCATION: (101
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LOCATION: (10)
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NAME/KEY: CDS
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236761
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US-10-928-446A-183/C

Sequence 183, Application US/10928446A

Publication No. US20050277123A1

SEQUENCE INCORNATION:

APPLICANT: UNIVERSITY OF UTAH RESEARCH FOUNDATION

TITLE OF INVENTION: VARIANTS OF NEDD-IA ASSOCIATED WITH HYPERTENSION AND

TITLE OF INVENTION: VIRAL BUDDING

TITLE OF INVENTION: VARIANTS OF NEDD-IA ASSOCIATED WITH HYPERTENSION AND

TITLE OF INVENTION: VARIANTS OF NEDD-IA ASSOCIATED WITH HYPERTENSION AND

TITLE OF INVENTION: VARIANTS OF NEDD-IA

CURRENT APPLICATION NUMBER: US/10/928,446A

CURRENT FILING DATE: 2002-02-6

NUMBER OF SEQ ID NOS: 202

SOFTWARE: PATENTIN Ver. 2.1

SEQ ID NO 183

LENGTH: 1080000
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                                                                                                                                                                                                                                                                                                                         DB 6; Length 1080000;
                                                                                                                                                                                                                                                                                                                                                                    84; Indels
                                                                                                                                                                                                                                                  ) OTHER INFORMATION: full exon 30 range is 1073289-1075279 US-10-928-446A-181
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                                                                                                                                                                                                                                                                                                                     Score 36.6; DB; Pred. No. 78; 0; Mismatches
                                                                FEATURE:
NAME/KEY: CDS
LOCATION: (1068609) .. (1068681)
COTHER INFORMATION: exon
FEATURE:
NAME/KEY: CDS
LOCATION: (1073289) .. (1073388)
NAME/KEY: CDS
LOCATION: (1067768)..(1067864)
OTHER INFORMATION: exon
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LOCATION: (929123)..(929176)
OTHER INFORMATION: exon
FEATURE:
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NAME/KEY: CDS
LOCATION: (826985)..(827017)
FEATURE:
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OTHER INFORMATION: exon
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OTHER INFORMATION: exon
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ORGANISM: Homo sapiens
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LOCATION: (84)
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NAME/KEY: CDS
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NAME/KEY: CDS
LOCATION: (1043121)..(1043350)
COTHER INFORMATION: exon
FEATURE:
NAME/KEY: CDS
LOCATION: (1044868)..(1044989)
OTHER INFORMATION: exon
FEATURE:
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LOCATION: (1050296)..(1050391)
OTHER INFORMATION: exon
FEATURE:
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NAME/KEY: CDS
LOCATION: (1000354)..(1000456)
OTHER INFORMATION: exon
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NAME/KEY: CDS
LOCATION: (1002118)..(1002284)
OTHER INFORMATION: exon
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LOCATION: (1006117)...(1006249)
OTHER INFORMATION: exon
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LOCATION: (1007860)..(1008036)
JTHER INFORMATION: exon
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LOCATION: (1010940)..(1011014)
JTHER INFORMATION: exon
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COCATION: (1018160)..(1018291)
JTHER INFORMATION: exon
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LOCATION: (1028113)..(1028167)
OTHÈR INFORMATION: exon
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COCATION: (1034316)..(1034374)
OTHER INFORMATION: exon
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LOCATION: (1020028)..(1020225)
THER INFORMATION: exon
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LOCATION: (1026659)..(1026736)
OTHER INFORMATION: exon
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LOCATION: (1047519) .. (1047589)
OOTHER INFORMATION: excn
FEATURE:
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LOCATION: (1018800)..(1018919)
OTHER INFORMATION: exon
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OTHER INFORMATION: exon
                                                            FEATURE:
NAMESKEY: CDS
LOCATION: (999547)..(999608)
OTHER INFORMATION: exon
NAME/KEY: CDS .
LOCATION: (993104)..(993154)
OTHER INFORMATION: exon
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236700 AGACTGGGTTTCACCATGTTGGCCAGGCTGGTCTCAAACTCCTGACCTTAG 236650

Search completed: December 30, 2005, 04:23:29 Job time : 941 Becs

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2.0%; Score 36.6; DB 6; Length 1080000;
Best Local Similarity 50.9%; Pred. No. 78;
Matches 87; Conservative 0; Mismatches 84; Indels 0; C
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US-10-928-446A-183
                                                                          NAME/KEY: CDS
LOCATION: (1062708)
OTHER INFORMATION: exon
PEATURE:
LOCATION: (1064561)
OTHER INFORMATION: exon
OTHER INFORMATION: exon
LOCATION: (1060368)..(1060441)
OTHER INFORMATION: exon
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LOCATION: (1066207)..(1066314)
OTHER INFORMATION: exon
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OTHER INFORMATION: exon
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LOCATION: (1068609)..(1068681)
OTHER INFORMATION: exon
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LOCATION: (1073289)..(1073388)
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AC138308 Mus muscu CR385039 Zebrafish

AC134480 AC138308 CR385039

	Description	BC013549 Mus muscu	AF361644 Mus muscu	AK220209 Mus muscu	AC117716 Mus muscu	AC074220 Mus muscu	AC134482 Rattus no	AC131887 Rattus no	AC135655 Rattus no	CQ921127 Sequence	AX198865 Sequence	AX209392 Sequence	AF161347 Homo sapi	BC022093 Homo sapi	AR379595 Sequence	BC008133 Homo sapi	BC008898 Homo sapi	BC008961 Homo sapi	BC011767 Homo sapi
SUMMAKIES	ΩI	BC013549	AF361644	AK220209	AC117716	AC074220	AC134482	AC131887	AC135655	CQ921127	AX198865	AX209392	AF161347	BC022093	AR379595	BC008133	BC008898	BC008961	BC011767
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	ALIGNMENTS	\	N BC013549 BC013549.1 GI:15488835 MGC. Mus musculus (house mouse) SM Mus musculus	:		Scheer, 1.E., Browner L., 1.E., Loguellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McEwan, P.J., McEwan, P.J., McEwan, P.J., McEwan, P.J., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Hellton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,	Dickson,M.C., Rodriguez,A.C., Grlmwood,J., Schmutz,J., Myers,K.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.		
:		RESULT 1 BC013549 LOCUS DEFINITION	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	20 20 20 20 20 20 20 20 20 20 20 20 20 2	AUTHORS		į	JOURNAL	REFERENCE AUTHORS TITLE JOURNAL

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                                                    WIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbbe-r@mail.nih.gov
Tissue Procurement: Jefferey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web Bite:
(Dickson, Mark) mcd@paxil.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Bickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
R. M.
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 31982623.
Location/Qualifiers
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/clone="MGC:19340 IMAGB:4222133"
/tissue_type="Kidney, normal. 5 n
/clone_lib="NKI CGAP_Kid14"
/lab_host="DH10B"
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/product="trinucleotide_rep
/protein_id="AAM13549.1"
/db_xref="G1:15488836"
/db_xref="GeneID:72029"
/db_xref="GeneID:72029"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
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/note="synonyms: CAG4A,
/db_xref="GeneID:72029"
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Blocak,M.M., Li,Y., Reuille,R. and Rogers,M.B.
Direct Submission
Submitted (15-MAR-2001) Biology, University of South Florida, 4202
E. Fowler Avenue, Tampa, FL 33620, USA
Location/Qualifiers
1. 1909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                temales and male animals carrying an X chromosome derived
from a feral mouse (McBurney & Rogers, Dev. Biol., 89,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Sciurconathi; Murcidea; Muridae; Musinae; Mus.
1 (bases 1 to 1909)
Glozak, M.A., Li, Y., Reuille, R., Kim, K.H., Vo, M.N. and Rogers, M.B.
Trapping and characterization of novel retinoid response elements
Mol. Endocrinol. 17 (1), 27-41 (2003)
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AGAACTTCCAGGACAAACTCGGGTGTGGCACAAAGGGGCTGGACGCCAGAGCCAGAGCCA
                                   CGCCAGAGACTGCAGAGGGCACCTGACCTAACCCCCTGGAAAGCCAATCTGCAGTTC
                                                    CGCCAGAGACTGCAGAGAGAGGCACCTGACCCTAACCCCCCTGGGAAGCCAATCTGCAGTTC
                                                                                                    CCGTGTCCACCCCCTCCTGAGGACGCCTCATGCTCTGCCCAGCCCTTCTCCCAGGGC
                                                                                                                       CGGGTCCACCCACTCCTCTGAGGACGCCTCATGCTCTGCCCAGCCCTTCTCCCAGGGC
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/mol_type="mRNA"
/db_xref="taxon:10090"
/cbl_line="P19; derived from matings between C3H/He
/ccmll_line="P19; derived from gan X chromosome der
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/clone_lib="24 hr retinoic acid-treated P19 cDNA (B et al., Dev. Biol., 170, 420)"
9. 919 /codon start=1
/product="putative retinoic acid-regulated protein"
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942

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LPSKCEVCKYVAVVELKSAFEETGKYEKVIDTGYGILDGKGSGVKYTKSDIRLIEVTET
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ASLGGKKSKKKRSGVKGSSSGSSKQRKELGGLGEDANAEEEEGVQKASPLPHSPPDEL

128 162 188 222 248 282 308 342 368 402 428 462 488 522 548 582 608 642 668 702 728 762 788 822 848 882

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JOURNAL Submitted (22-FEB-2005) Hisashi Koga, Kazusa DNA Research Institute, Laboratory for Genome Informatics; 2-6-7 Kazusa-kamatari, Kisarazu, Chiba, 292-0818, Japan (E-mail:mouse@kazusa.or.jp, Tel:81-438-52-3919, Fax:81-438-52-3918) Location/Qualifiers 11655 11655	Ouery Match Query Match Suitaity 9.7%; Pred. No. 0; Matches 677; Conservative 0; Mismatches 2; Indels 0; Gaps 0; QY 157 GCGGGGCTGAGGAGCTGCTGCTTGCCCAGCAATGCGAAGTGTGCAAGTA 157 GCCGGGCTGAGGACCCACTGCGTTGCCCAGCAATGCGAAGTGTGCAAGTA CCGGGCTGAGGAGCCGACTGCGTTTGCCCAGCAAATGCGAAGTGTGCAAGTA QY 217 GTTGCTTGTGAGGAGCCGATTTGAGGAAACGGGAAAGTGTGAAGTATC CQY 217 ACCGGCTATGGCATCGGCTTTTGAGGAAACAGGAAAGTGAGAAGTTGAC QY 277 ACCGGCTATGGCATCGGAAGGGCTTTTGAGGAAACAGGAAGTACAGTACGAATTGAC QY 277 CGGCTATGGCATCGGAAGGGCTTTTGAGGAAACAGGAAAGGAAGTACAGGAAGTTA QY 277 CGGCTATGGCATCGGAAGGGCTTTTGAGGAAACAGGAAAGTACAGGAAGTTAAATTGAAGAAGAGAAGAGAAAAGAGAAAAGAGAAGTTAAATTGAAGAA	0y 397 GAGAGGACTGGCAACCGGTTTGCCAAGGGTATGTCGGAGACCTTTGAGACGCTGCAC 456 1
0y 909 AAGACCCCTGACTTCAGAGCTTGGGACACGCAGCGCAGC	Oy 1329 AGAACTTCCAGGACAAACTCGGGTGTGGCACAAAGGGCTGGACGCAGAGCCAGAGCCA 1388	AK220209 LOCUGS AK220209 LOCUGS AK220209 AK220209 AK220209 AK220209 AK220209 AK220209. AKZ20209. AKZANANANANANANANANANANANANANANANANANANA

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Research, 320 Charles Street, Cambridge, MA 02141, USA
On Dec 20, 2002 this sequence version replaced gi:20128494.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                       NOTE: This record contains 88 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will be preserved.
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Baria, N., Bastlen, V., Bloom, T., Boqualavkiy, L., Burkhgalter, B., Erown, A., Camarata, J., Campopiano, A., Chang, J., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Kells, C., Lancycque, K., Lamazares, R., Lancdonald, P., Major, J., Marquis, N., Mathews, C., McCarthy, M., McEwan, P., McRornan, K., Mellad, J., Mathews, C., McCarthy, M., McEwan, P., McRornan, K., Meldrim, J., Mathews, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Connor, T., O'Donnell, P., O'Connor, T., O'Donnell, P., O'Connor, T., O'Connell, P., O'Connell, P., O'Connell, P., O'Connell, P., O'Connell, P., O'Connell, P., O'Connell, R., Schauer, S., Schugbeck, R., Stance, R., Schugbeck, R., Schauer, S., Schugbeck, R., Stance, R., Schugbeck, R., Vol, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Voll, M., Nobel, R., Wol, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Whitter, M., Wold, R., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Whitter, M. Derbek, L., Zimmer, A. and Zody, M. Terit, Leafer, R., Releas, M., Travers, M., Terit, Leafer, R., Releas, M., Travers, M., Terit, L., Leafer, R., Subramen, M., Yon, Whitter, M., Willer, M. Terit, L., Leafer, R., Yong, G., Whitter, M., Willer, M., Man, M., Willer, M., Will
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                                                                                                                                                                                                                                                                                                            AC117716 108992 bp DNA linear HTG 20-DEC-2002
Mus musculus clone RP23-96H4, LOW-PASS SEQUENCE SAMPLING.
AC117716
                                                                  601 GGCTCCTCCAGTGGCAGCAAGCAAGCAAAGAAACTGGGGGGCCTGGGGGAGGATGCC 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 108992)
Birren, B., Nusbaum, C. and Lander, E.
Mus musculus, clone RP23-96H4
                                                                                                                                                                                                                                                                                                                                                                                                                       AC117716.2 GI:27311376
HTG: HTGS PHASE0.
Mus musculus (house mouse)
                                                                                                                                                                             661 AACGCCGAGGAGGAGGAGG 679
                                                                                                                                             817 AACGCCGAGGAGGAGG 835
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jnpublished
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50305 AGGCTATGTCGGAGACCTTTGAGACGCTGCACAACCTAGTCCACAAAGGGGTCAAGGTGG 50364

545 AGCAG 549 ||||| 50425 AGCAG 50429

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50424

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gap of 100 bp
contig of 1159 bp in length
gap of 100 bp
contig of 1155 bp in length
gap of 100 bp
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contrig of 11/1 c.
gap of 100 bp
c. of 1166 bp in length
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contig of 1148 bp in length
gap of 100 bp
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gap of 100 bp
contig of 1152 bp in length
gap of 100 bp
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of 1171 bp in length
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of 1167 bp in length
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of 1166 bp in length
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68495
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AC074220 89855 bp DNA linear HTG 15-MAY-2002 Wis musculus strain C57BL6/J chromosome 17 clone RP23-76116, WORKING DRAFT SEQUENCE, 38 unordered pieces.
                                                                                                                                                                                                                                                             Han, J., Montgomery, K.T., Grills, G., Lee, E., Long, J., Pomerantz, R., Ioshikhes, I.E., Shim, C., Decker, J., Thomas, E., Perera, A., Gordon, M., Goltz, J.S. and Kucherlapati, R.
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (20-JUL-2000) Department of Molecular Genetics, Albert, Instein College of Medicine Genome Center, 1300 Morris Park Ave., Bronx, NY 10461, USA Genome Center, On Apr 28, 2001 this sequence version replaced gi:11276104.
                                                                                                                                                                                                                                                                                                                                                                                                                              Pomerantz, R.,
                                                                                                                                                                                                        Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality coverage: agarose-FP - N/A Quality coverage: 5.1 x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      arbitrary, Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              * NOTE: This is a 'working draft' sequence. It currently a consists of 38 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                           Han,J., Montgomery,K.T., Grills,G., Lee,E., Long,J., Pome:
Ioshikhes,I.P., Shim,C., Decker,J., Thomas,E., Perera,A.,
Gordon,M., Goltz,J.S. and Kucherlapati,R.
Direct Submission
                                                                                                                                                                                        Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; But
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 89855)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2: contig of 7962 bp in length
2: gap of unknown length
4: contig of 5942 bp in length
5: contig of 5946 bp in length
6: contig of 5046 bp in length
7: gap of unknown length
7: contig of 3491 bp in length
6: gap of unknown length
7: contig of 4556 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: Harvard Partners Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ------Genome Center
                                                                                                                      AC074220.7 GI:13876390
HTG; HTGS PHASE1; HTGS DRAFT.
Mus musculus (house mouse)
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13924:
13944:
18990:
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KEYWORDS
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AUTHORS
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RESULT
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Indels

6.8%; Score 125; DB 14; ilarity 100.0%; Pred. No. 4.7e-59; Conservative 0; Mismatches 0;

Best Local Similarity Matches 125; Conserv

Query Match

Length 108992;

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gap or unknown length

2: contig of 2076 bp in length

3: gap of unknown length

3: contig of 1817 bp in length

3: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     770 86770: contig of 1001 bp in length
771 86790: gap of unknown length
78207: contig of 1417 bp in length
88227: gap of unknown length
8827: contig of 749 bp in length
997 88955: contig of mknown length
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                  f 810 bp in length
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f 2335 bp in length
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/mol type="genomic DNA"
/strain="C57BL6/J"
/db xref="taxon:10090"
/chromosome="17"
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source
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Query Match 5.4%; Score 99; DB 14; Length 89855; Best Local Similarity 100.0%; Pred. No. 3.8e-44; Matches 99; Conservative 0; Mismatches 0; Indels 0
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3925. .13944
                                                                                                                                                                                           estimated length=unknown
9011. .22501
note="assembly_name:Contig142"
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note="assembly_name:Contig140"
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estimated length=unknown
18840. .31224
note="assembly_name:Contigl39"
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'estimated length=unknown
'5114. .38611
'note="assembly_name:Contig137"
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17080. .49496
17081 - asssembly_name:Contigl33"
19497. .49516
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9517. .52236
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estimated_length=unknown
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estimated length=unknown
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clone="RP23-76116"
sex="male"
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9 GGAGGAAGCGCCGCCGGCTCCGCTCTGGTCCGGCTGGGCCATGGAGTCCATGTC 68

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(bases 1 to 222256)
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Schrödgraft, Marziczej Marziczej, Mann, A., Angulano, D.,
Allan, C., Allen, A., Alboroke, S., Mann, A., Angulano, D.,
Allan, C., Allen, H., Alboroke, S., Mann, A., Angulano, D.,
Allan, C., Allen, H., Alboroke, S., Mann, A., Angulano, D.,
Baldwin, D., Bandaranaike, D., Barzber, M., Barazed, M., Benahmed, F.,
Baldwin, D., Blandaranaike, D., Barzber, M., Barazed, D., Brown, M.,
Bryant, N., Bular, J., Blankenburg, K., Blyth, P., Brown, M.,
Bryant, N., Bulay, C., Burch, P., Burrell, K., Cater, A., Chenz, C., Corder, A.,
Clacdens, V., Carter, K., Cavazo, I., Cesar, H., Divaz, L.,
Clacdeland, C., Cockrell, R., Cox, C., Coyle, M., Cree, D. D'Genzal, L.,
Bavila, M.L., Durson, S., Deramo, C., Didy, M., Durchin, K., Duval, B., Eaves, K.,
Bryant, M., Bugen, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
Drager, H., Dugnen, Rocha, S., Dunn, A., Durchin, K., Duval, B., Eaves, K.,
Brander, S., Finley, M., Bugen, C., Forles, L., Foster, M., Forster, M.,
Eraser, C.M., Gabisi, M., Gans, R., Garza, M., Garza, M.,
Gebreggeorger, S., Filley, M., Gans, R., Garza, M.,
Harvey, Y., Havlak, P., Hawse, A., Hanil, C., Hamilton, C., Hamilton, C., Hamilton, C., Hanilton, C., Harinandez, R., Harsey, S., Kelly, S., Hune, J., Marzander, M., Marzen, M., Shurker, M., Shurken, M., 
                                                                                                                                                                                                                                                                     222256 bp DNA linear HTG 15-NOV-2002
Rattus norvegicus clone CH230-179K4, *** SEQUENCING IN PROGRESS
***, 2 unordered pieces.
6070 GGAGGAAGCGCCGCCCGCTCTCTCTCTCTCGCTCCGCCTGGGCCATGGAGTCCATGTC 6011
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Mammalia, Butheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Rattus.
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HTG; HTGS PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
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AC134482
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Submitted (15-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA, On Nov 15, 2002 this sequence version replaced gi:23334632. On Nov 15, 2002 this sequence version replaced gi:23334632. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bom.unc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads.
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NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                        Submitted (27-SEP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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3.8%; Score 69; DB 14; Length 222256;
Best Local Similarity 100.0%; Pred. No. 6.1e-27;
Matches 69; Conservative 0; Mismatches 0; Indels 0;
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Contact: hgsc-help@bcm.tmc.edu
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/mol_type="genomic DNA"
/db_xref="taxon:10116"
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Rat Genome Sequencing Consortium.
Rat Genome Sequencing Consortium.
Direct Submission
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107900. .107999
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AC131887 246404 bp DNA linear HTG 09-MAY-2003
Rattus norvegicus clone CH230-3M14, WORKING DRAFT SEQUENCE, 3
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Rattus.
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Rattus norvegicus (Norway rat)
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AC131887.3 GI:30466855
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KEYWORDS
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AC131887 RESULT 7

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Submitted (09-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA on May 9, 2000 This sequence versaion replaced gi:2370097.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.imc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads.
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                                                                 Direct Submission
Submitted (27-AUG-2002) Human Genome Sequencing Center, Department
Submitted (27-AUG-2002) Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 246404)
Rat Genome Sequencing Consortium.
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Consensus quality: 240099 bases at least Q30
Consensus quality: 241516 bases at least Q30
Consensus quality: 241516 bases at least Q30
Estimated insert size: 249377; aum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
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8 161357: gap of unknown length
8 188568: contig of 27211 bp in length
9 188668: gap of unknown length
9 246404: contig of 57736 bp in length.
Location/Qualifiers
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Contact: hgsc-help@bcm.tmc.edu
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/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-3M14"
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Center clone name: CH230-3M14
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Rat Genome Sequencing Consortium.
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                                                                                                                                                                AC135655 270958 bp DNA linear HTG 20-NOV-2002 Rattus norvegicus clone CH230-6908, *** SEQUENCING IN PROGRESS ***, 4 unordered pieces.
                                                                     ö
                                                                                                                                676 GCAGAGCGGTGGTCTGGCAAGAAGAAGGCGACATAGCCTCCCTGGGAGGAAGAAATCCAAG 735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
                                                                     0; Gaps
3.8%; Score 69; DB 14; Length 246404;
100.0%; Pred. No. 6.2e-27;
tive 0; Mismatches 0; Indels 0;
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
                                     1 Similarity 100.
69; Conservative
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            Query Match
Best Local &
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Submitted (20-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 20, 2002 this sequence version replaced gi:24158508.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
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NOTE: This is a "working draft' sequence It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                             Chases 1 to 270958)

Att Genome Sequencing Consortium.

Direct Submission

Submitted (20-OCT-2002) Human Genome Sequencing Center, Department

of Molecular and Human Genetics, Baylor College of Medicine, One

Baylor Plaza, Houston, TX 77030, USA

3 (Dases 1 to 270958)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von
Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
Weinstock,G. and Gibbs,R.A.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Center code: BCM
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Direct Submission
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/db_xref="taxon:10116"
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91405. .94036
/note="wgs_contig"
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
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2.7%; Score 50; DB 6; Length 526;
Best Local Similarity 100.0%; Pred. No. 3.7e-16;
Matches 50; Conservative 0; Mismatches 0; Indels
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2.7%; Score 50; DB 6; Length 580;
Best Local Similarity 100.0%; Pred. No. 3.7e-16;
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Patent: WO 0151513-A 1320 19-JUL-2001;
CORIXA CORPORATION (US)
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
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/note="n includes a, c,
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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Methods for prognosis and treatment of solid tumors
Patent: WO 2004097052-A 2327 11-NOV-2004;
Wyeth (US); Burczynski, Michael E. (US)
Location/Qualifiers
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102157. .101191

/note="wgg contig"

24279387

/note="wgg contig"

246116. .248554

/note="wgg contig"

248555. .248654

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248655. .249752

/note="wgg contig"

267830. .267929

267830. .267929

/estimated_length=unknown

26947. .269046

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Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
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Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
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Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Butterfield, Y.S., Krzywinski, M.I., Skalaka, U., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalaka, U., Smailus, D.E.,
Schnerch, A., Schein, J. E., Jonses, S.J. and Marra, M.A.
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                                                                                                                                                                                                                                                                                                                                          904 bp mRNA linear PRI 07-NOV-2003
Homo sapiens trinucleotide repeat containing 5, mRNA (cDNA clone
IMAGE:3534003), partial cds.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Submitted (22-JAN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadandsystemsbiology.org
Anup Madan, Jessica Pahey, Erin Helton, Mark Ketteman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
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NIH-MCC Project URL: http://mgc.nci.nih.gov
ON Nov 6, 2003 this sequence version replaced gi:18314384.
Contact: MGC help desk
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                              Length 612;
                       2.7%; Score 50; DB 8; Lt
100.0%; Pred. No. 3.7e-16;
iive 0; Mismatches 0;
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/organism="Homo sapiens"
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Tissue Procurement: DCTD/DTP
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hvlkgkdtsclaeqwsgkkgdtaalggkkskkkssrakaaggrsssskqrkelgglre
tpaprrmrasrrhplshtaplmsseptqhpvlrpsslkse"
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1 (Dases 1 to 612)
Zhang, Q.H., Ye, M., Zhou, J., Shen, Y., Wu, X.Y., Guan, Z.Q., Wang, L., Fan, H.Y., Mao, Y.F., Dai, M., Huang, Q.H., Chen, S.J. and Chen, Z. Human partial CDS cloned from cd34+ stem cells
Unpublished

2 (Dases 1 to 612)
2 (Dases 1 to 612)
2 (Dases 1 to 612)
2 (Dases 2 to 612)
2 (Dases 3 to 612)
3 (Dases 3 to 612)
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5 (Dases 5 to 612)
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6 (Dases 7 to 612)
7 (Dases 7 to 612)
8 (Dases 7 to 612)
8 (Dases 8 to 612)
8 (Dases 9 to 612)
8 (Dases 9 to 612)
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9 (Dases 1 to 613)
9 (Dases 1
                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
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100.0%; Pred. No. 3.7e-16;
tive 0; Mismatches 0; Indels
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Homo sapiens HSPC084 mRNA, partial cds.
AF161347
      DNA
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CORIXA CORPORATION (US)
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<1. 431
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AX209392
Sequence 1232 from Patent WO0157207.

    .580
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TITLE

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Straubberg, L., Feingold, B.A., Grouse, L.H., Derge, J.G., Ratauberg, R.L., Feingold, B.A., Grouse, L.H., Derge, J.G., Altschul, S.P., Collins, F.S., Wagner, L., Shemmen, C.M., Schuler, G.D., Altschul, S.P., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Uddin, F. H., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McBwan, P.J., McKernan, K.J., Malek, J.A., Gunartane, P.H., Richards, S.W., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Lu, X., Gibbs, R.A., Villaion, D.K., Muzny, D.M., Sodergren, B.J., Lu, X., Gibbs, R.A., Banchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G., Blakesley, R.W., Touchman, J.W., Green, E.D., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Sanilus, D.E., Schnetz, J., Myers, R.M., Schein, J. B., Jones, S.J. and Marra, M.A.
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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (22-MAY-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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100.0%; Pred. No. 3.8e-16;
ive 0; Mismatches 0;
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/clone Tib="NIH MGC_12"
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/organism="Homo sapiens"
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/clone="IMAGE:3457829"
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//translation="VVMDIPYELWHETSAEVADLKKQCDVLVBEFEEVIEDWYRNHQE
ED.TreficahHVLKREDTSCLAEQWSGKKGPTAALGGKKSKKKSSRAKAAGGRSSSSK
QRKELGGLEGDPSPEEDEGIQKASPLTHSPPDEL"
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unclassified.

1 (bases 1 to 1201)

Cocks B.G. Stuart, S.G. and Seilhamer, J.J.

Cocks B.G. Stuart, S.G. and Seilhamer, J.J.

Compositions for the detection of blood cell and immunological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                      /tissue_type="Lung, small cell carcinoma"
Clone_lib="NTH WGC 7"
(lab_host="DH10B-R"
note="Vector: pOTB7"
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3.8e-16;
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Homo sapiens cDNA clone IMAGE:3457829.
BC008133
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Patent: US 6607879-A 140 19-AUG-2003;
Incyte Corporation; Palo Alto, CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AR379595 1201 bp DN
Sequence 140 from patent US 6607879.
AR379595
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-ive 0; Mismatches
                                                                                                                                                                                                                                                                               /product="TNRC5 protein"
/protein id="AAH22093.3"
/db_xref="G1:38196971"
                                                                                                                                             /gene="TNRC5"
/note="synonyms: ERDA5,
/db_xref="GeneID:10695"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="genomic DNA"
db_xref="taxon:9606"
clone="IMAGE:3534003"
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Homo sapiens
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Best Local Similarity 100.
Matches 50; Conservative
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VERSION
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TITLE
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Ada45654
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Ada613138
Ada613138
Ada673108
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Scoring table:

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Trinucleotide repeat protein; TRP; T243; embryonic stem cell; ES; transgenic animal; knockout mouse; triplet repeat expansion; fragile X syndrome; Huntington's disease; mouse; murine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Murine trinucleotide repeat protein (TRP) cDNA sequence.
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ACA04091
ADA45554
ADA46085
ADA61358
ADA19133
ADB27684
ADA919133
ADA76138
ADA91575
ADA47513
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/product= "TRP"
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P-PSDB; AAU02498.
WO200130798-A1.
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 AAS05278;
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 Aa805278 Murine tr
Aa805286 DNA seque
Adv7441 Nucleotid
Aa805289 DNA seque
Ad188397 DNA up-re
Ad188395 DNA up-re
Ad188396 DNA up-re
Ad23979 Human Gen
Adv11888 Solid tum
Aa825051 Human ova
Adv1188 Solid tum
Aa825051 Human ova
Adv1184 Human NTR
Adi3081 Human CDN
Adm7164 Human CDN
Adm3081 Human LYM
Adu82624 Human MDD
Aa805279 Human Lri
Aca54677 Human NF-
Adu83175 Human tri
                                                                                               ; Search time 1051 Seconds (without alignments)
11661.627 Million cell updates/sec
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                5.1.6
Compugen Ltd.
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                GenCore version (c) 1993 - 2005
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AACS05284
AATZ3979
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Gapop_60.0 , Gapext 60.0
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11: geneseqm1980s:*
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4: geneseqm2001as:*
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1839
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Match
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Novel transgenic animals useful as animal model for characterization of function of a gene encoding trinucleotide repeat proteins (TRPs), contains heterozygous disruption in a gene encoding TRP.

Claim 8; Fig 11; 106pp; English

ACA54677 ADU83175

1201 1201 1226 1362 1378

11888 11888 11828

Score

Result

The present sequence encodes for murine trinucleotide repeat protein (TRP). The invention describes methods of producing embryonic stem (ES) cells comprising a heterozygous disruption in a target DNA sequence (preferably gene T243) encoding a TRP and of producing a knockout mouse comprising a homozygous disruption in a gene encoding TRP, where the comprising a homozygous disruption in the wild type TRP. The invention also relates to identifying agents capable of affecting a phenotype of a knockout mouse. Also described are methods of determining whether concept the trinucleotide repeat in a gene encoding TRP produces a phenotypic change. The transgenic animals and the cells are useful for identifying compounds capable of ameliorating disease symptoms, and as test substrates for the identification of drugs, pharmaceuticals, therapies and interventions which may be effective in treating trinucleotide repeat disorders e.g. fragile X syndrome and Huntington's disease. The animal models for trinucleotide repeat disorders are ideal condel systems to study the progression of disease in vivo, the molecular basis of these diseases and show the features observed in human disease. Using the mice, it is possible to model both the pathogenic mechanism and the trinucleotide repeat instability in the mouse

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Sequence 1839 BP; 424 A; 522 C; 535 G; 358 T; 0 U; 0 Other;

480 480 540 240 240 540 900 600 99 999 720 720 120 180 180 300 360 360 420 420 TCCATGTCTGAGCTCGCGCCCCCGCTGCCTCTTATTTCCTTTGCTGCTGCTGCTTCCGCTG 120 300 9 AAGGGCTCTGGAGTCAAGTACACCAAGTCGGACTTACGGTTAATTGAAGTCACTGAGACC GACACGAGTTGCCTAGCAGAGCGGTGGTCTGGCAAGAAGGGGGACATAGCTCCCTGGGA GGCACGAGGGAGGAAGCGCCGCCCGGGTCCGCTCTGCTCTGGGTCCGGCTGGGCCATGGAG GGCACGAGGGAGGGGCGCCGGGTCCGCTCTGCTCTGGGTCCGGCTGGGCATGGAG TCCATGTCTGAGCTCGCGCCCCGCTGCCTCTTATTTCCTTTGCTGCTGCTGCTTCCTCTG CTGCTCCTTCCTGCCCCGAAGCTAGGCCCGAGTCCCGCGGGGCTGAGGAGACCGACTGG CTGCTCCTTCCTGCCCCCGAAGCTAGGCCCGAGTCCCGCCGGGGCTGAGGAGAGACGACTGG GTGCGATTGCCCAGCAAATGCGAAGTGTGCAAGTATGTTGCTGTGGAGCTGAAGTCGGCT GTGCGATTGCCCCAGCAAATGCGAAGTGTGCAAGTATGTTGCTGTGGAGCTGAAGTCGCC TITGAGGAAACGGGAAAGACCAAGGAAGTGATTGACACCGGCTATGGCATCCTGGACGGG rtrigaggaaacgggaagaccaaggaagrgarrgacaccggcrarggcarccrgacgg AAGGGCTCTGGAGTCAAGTACACCAAGTCGGACTTACGGTTAATTGAAGTCACTGAGACC ATTTGCAAGAGGCTTCTGGACTACAGCCTGCACAAGGAGAGGACTGGCAGCAACCGGTTT GCCAAGGGTATGTCGGAGACCTTTGAGACGCTGCACAACCTAGTCCACAAAGGGGTCAAG GCCAAGGGTATGTCGGAGACCTTTGAGACGCTGCACAAACCTAGTCCACAAAAGGGGTCAAG GTGGTGATGGATATCCCCTATGAGCTGTGGAACGAGACCTCAGCAGAGGTGGCTGACCTC Greerearceararcecerareacereresaaceacereaceacadadeacereacere AAGAAGCAGTGTGTGCTGGTGGAAGAGTTTGAAGAGGTGATTGAGGACTGGTACAGG AACCACCAGGAGGAAGACCTGACTGAATTCCTCTGTGCCAACCACGTGCTGAAGGGAAAG GACACGAGTTGCCTAGCAGAGCGGTGGTCTGGCAAGAAGGGGGAACATAGCCTCCCTGGGA Gaps ô DB 4; Length 1839; IndelB . 0 100.0%; Score 1839; 100.0%; Pred. No. 0; ive 0; Mismatches Query Match Best Local Similarity 100. Matches 1839; Conservative н 61 121 121 181 181 241 241 301 301 361 361 421 481 541 541 601 601 661 661 61 421 481

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The present sequence represents the DNA sequence of an expanded T243

gene. The T243 gene encodes for a trinucleotide repeat protein (TRP). The invention describes methods of producing embryonic steem (ES) cells

comprising a heterozygous disruption in a target DNA sequence (preferably gene T243) encoding TRP and of producing a knockout mouse comprising a homozygous disruption in a gene encoding TRP, where the disruption in in a gene encoding TRP. The invention also relates to identifying agents capable of affecting a phenotype of a knockout mouse. Also described are methods of determining whether expansion of the trinucleotide repeat in a gene encoding TRP produces a phenotypic change. The transgenic animals and the cells are useful for identifying compounds capable of ameliorating disease symptoms, and as test substrates for the identification of drugs, pharmaceuticals, therapies and interventions which may be effective in treating trinucleotide repeat disorders e.g. fragile X syndrome and Huntington's disease. The animal models for trinucleotide repeat disorders are ideal model systems to study the progression of disease in vivo, the molecular basis of these diseases and show the features observed in human disease. Using the mice, it is possible to model both the pathogenic mechanism and the trinucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel transgenic animals useful as animal model for characterization of function of a gene encoding trinucleotide repeat proteins (TRPs), contains heterozygous disruption in a gene encoding TRP.
                                                                                                                                                                                                                                                                        ES;
                                                                                                                                                                                                                                                                      embryonic stem cell;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1848 BP; 415 A; 519 C; 543 G; 371 T; 0 U; 0 Other;
                              Allen KD;
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Score 1658; DB 4; Length 1848;

90.2%; Score 1658; I 100.0%; Pred. No. 0;

Query Match Best Local Similarity

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Novel gene encoding protein involved in fibroblast growth factor signal transduction, useful for analyzing mechanism of formation of organs such as midbrain optic-tectum portion, cerebellum, inner ear and canceration mechanism of cell.
                                                                                                                                                                         The present sequence encodes a protein involved in fibroblast growth factor (FGF) signal transduction. Such proteins are useful for analyzing the mechanism of formation of various organs, such as midbrain optictectum portion by a midbrain mesencephalon border, the mechanism of formation of cerebellum. mechanisms of formation of inner ear, blood vessels. limb buds, teeth, and canceration mechanisms of a cell.
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Novel transgenic animals useful as animal model for characterization function of a gene encoding trinucleotide repeat proteins (TRPs), contains heterozygous disruption in a gene encoding TRP.

Disclosure, Fig 15; 106pp; English.

ğ Allen

Moore M,

Klein R, Matthews W, (DELT-) DELTAGEN INC

WPI; 2001-300473/31.

26-OCT-2000; 2000WO-US029382

WO200130798-A1

03-MAY-2001

99US-0161488P

26-OCT-1999;

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                                              GGAACTGGGGGGGCCTGGGGGGATGCCAACGCCGAGGAGGAGGAGGAGGAGGTGTGT
                                                                                  ATCGCCCCTCCCACACACCCCCCTGATGAGCTGTGAGCCCCAGCTTAGTGCTTGAATC
                                                                                                              AAGACCCCTGACTTCAGAGCTTGGGACACGCACAGCGCAGCGCAGCGCAGCTCCAGCAAG
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The present sequence representing the DNA sequence of a deleted gene fragment of the target T443 gene is generated by using a construct comprising T443 homologous sequences (AASO5284-AASO5285). The T243 gene encodes for a trinucleotide repeat protein (TRP). The invention describes methods of producing embryonic stem (ES) cells comprising a hererozygous distruption in a target DNA sequence (preferably gene T243) encoding a TRP CC and of producing a knockout mouse comprising a homozygous distruption in a gene encoding TRP. The invention also relates to identifying agents capable of affecting a phenotype of a knockout mouse. Also described are methods of determining whether expansion of the trinucleotide repeat in a gene coding TRP produces a phenotypic change. The transgenic animals and the cells are useful for identifying compounds capable of ameliorating calsease symptoms, and as test substrates for the identification of drugs, characting trinucleotide repeat disorders e.g. fragile X syndrome and treating trinucleotide repeat disorders e.g. fragile X syndrome and Huntington's disease. The animal models for trinucleotide repeat covivo, the molecular basis of these diseases and show the features covivo, the molecular basis of these diseases and show the features construction mouse. The pathogenic mechanism and the trinucleotide repeat instability in the molecular parameter of the pathogenic mechanism and the trinucleotide repeat instability in the molecular.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.8%; Score 107; DB 4; Length 107; 100.0%; Pred. No. 4.5e-28; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCCGAAGCTAGGCCCGAGTCCCGCCGGGGCTGAAGAAAGCTAGGCCGACTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 107 BP; 9 A; 42 C; 31 G; 25 T; 0 U; 0 Other;
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Trinucleotide repeat protein; TRP; T243; embryonic stem cell transgenic animal; knockout mouse; triplet repeat expansion; fragile X syndrome; Huntington's disease; mouse; mutant; ds.

Mus sp. Synthetic.

DNA sequence of deleted gene fragment of target T243 gene.

(first entry)

07-SEP-2001

X S S X K K K K E X L X Y X

AAS05289 standard; DNA; 107

AAS05289

RESULT

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This invention relates to a novel method for predicting gene potential by associating nucleic acid sequences of unknown function with particular cub-poulation profiles. Specifically, it refers to classifying an unknown multi-lineage affiliated gene by collecting hybridisation data to develop a gene expression map, in order to determine the discrete subcopulation where it is expressed. The present invention describes methods for predicting the lineage commitment of genes associated with the self-renewing haematopoietic (blood) stem cells (HSCs), as well as the nonself renewing multipotent progenitors (CMPs), common lymphoid progenitors (CLPs) and common myeloid progenitors (CMPs), which are collectively referred to as bone marrow stem cells populations. As such, these methods can be used to identify associated multi-lineage affiliated genes and hence the underlying molecular mechanisms in physiological haematopoietic development. This polynucleciide sequence is DNA associated with a murine HSC sub population of cells of the invention.
                                                                                                                                                                                     Classifying an unknown multi-lineage affiliated gene comprises isolating expressed nucleic acid sequences from the discrete cell sub-populations.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Trinucleotide repeat protein; TRP; T243; embryonic stem cell; ES; transgenic animal; knockout mouse; triplet repeat expansion; fragile X syndrome; Huntington's disease; mouse; ds.
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100.0%; Pred. No. 1.4e-25;
ative 0; Mismatches 0;
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                                                                                                                                                                                                                                                               Claim 7; SEQ ID NO 4789; 123pp; English.
                                              (STOW-) STOWERS INST MEDICAL RES
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03-MAY-2002; 2002US-0377383P.
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                                                                                                                                           WPI; 2004-022656/02.
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Matches 100;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention relates to a novel method for predicting gene potential by associating nucleic acid sequences of unknown function with particular sub-population profiles. Specifically, it refers to classifying an unknown multi-lineage affiliated gene by collecting hybridisation data to develop a gene expression map, in order to determine the discrete sub-population where it is expressed. The present invention describes methods for predicting the lineage commitment of genes associated with the self-renewing multipotent progenitors (MPBs), common lymphoid progenitors (CLPs) and common myeloid progenitors (CMPs), which are collectively referred to as bone marrow stem cells populations. As such, these methods can be used to identify associated multi-lineage affiliated genes and hence the underlying molecular mechanisms in physiological haematopoietic development. This polymucleotide sequence is DNA associated with a murine
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                                                                                                                                                                                                                                                                                                                                                            Classifying an unknown multi-lineage affiliated gene comprises isolating expressed nucleic acid sequences from the discrete cell sub-populations.
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1.4e-25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 7; SEQ ID NO 4790; 123pp; English.
                                                                                                                                                                                                                (STOW-) STOWERS INST MEDICAL RES.
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                                                                                                                     05-MAY-2003; 2003WO-US014114.
                                                                                                                                                                 03-MAY-2002; 2002US-0377383P.
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                                                                                                                                                                                                                                                                                                                WPI; 2004-022656/02
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                                                                       13-NOV-2003
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Matches

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RESULT 6 ADL88396

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Gaps

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Length 100; Indels

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WPI; 1995-206931/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADU11888;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADU11888
CXSXLTTTXBXLLXXBXXLXXBXXXXXXXXXXCXXX
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                                                                                      The present sequence for T243 homologous sequence #1 is generated by PCR and is homologous to the T243 gene which encodes for a trinucleotide repeat protein (TRP). The invention describes methods of producing embryonic stem (ES) cells comprising a heteroxygous disruption in a carget DNA sequence (preferably gene T243) encoding TRP and of producing a knockout mouse comprising a homozygous disruption in a gene encoding TRP. The invention also relates to identifying agents capable of affecting a phenotype of a knockout mouse. Also described are methods of affecting a phenotype of a knockout mouse. Also described are methods of affecting a phenotype of a knockout mouse. Also described are methods of affecting a phenotype of a knockout mouse and the trinucleotide repeat in a gene encoding TRP produces a phenotypic change. The transgenic animals and the calls are useful for identifying compounds capable of ameliorating calsease symptoms, and as test substrates for the identification of drugs, pharmaceuticals, therapies and interventions which may be effective in treating trinucleotide repeat disorders e.g. fragile X syndrome and Huntington's disease. The animal models for trinucleotide repeat disorders are ideal model systems to study the progression of disease in vivo, the molecular basis of these diseases and show the features observed in human disease. Using the mice, it is possible to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 GGAGGAAGCGCCGCCGCCGCTCTGCTCTGGGTCCGGCTGGGCCATGGAGTCCATGTC 68
                                                                                                                                                                                                                                                                                                                                        observed in human disease. Using the mice, it is possible to model both the pathogenic mechanism and the trinucleotide repeat instability in the mouse
           Novel transgenic animals useful as animal model for characterization of function of a gene encoding trinucleotide repeat proteins (TRPs), contains heterozygous disruption in a gene encoding TRP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                 3.6%; Score 66; DB 4; Length 471;
100.0%; Pred. No. 1.1e-13;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 471 BP; 105 A; 129 C; 148 G; 88 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAT23979 standard; cDNA to mRNA; 189 BP.
                                                                  Claim 11; Fig 14; 106pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human gene signature HUMGS05940.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94WO-JP001916.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93JP-00355504.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matsubara K, Okubo K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MATSUBARA K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         466 TGAGCT 471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69 TGAGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-SEP-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                              A single-stranded DNA (or its complementary strand or the corresp. double stranded DNA) which comprises one of the 7837 "GS" sequences given in ART19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'- untranblated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell
Single-stranded DNA for identifying gene signatures - isolated from 3'-directed human cDNA library that reflects relative abundance of corresp. mRNA in specific human tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A method, useful for prognosing and treating solid tumor, comprises comparing an expression profile of a gene expressed in peripheral blood mononuclear cells to a reference expression profile of a gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              635
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 therapy; expression profile; solid tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 189 BP; 56 A; 44 C; 58 G; 21 T; 0 U; 10 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cytostatic; gene therapy; expression profile; solid tum
peripheral blood mononuclear cell; PBMC; prognosis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            function or for recognising different cell types
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100.0%; Pred. No. 6.2e-08;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Solid tumour prognosis gene seqid 2327.
                                                                                                                                                       Claim 1; Page 1501; 2245pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page; 111pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADU11888 standard; DNA; 526 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-APR-2003; 2003US-0466067P.
23-JAN-2004; 2004US-0538246P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strahs A, Trepicchio WL,
Immerman F, Dorner AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0
"...heg 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-JAN-2005 (first entry)
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(STRA/) STRAHS A.
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WPI; 2001-488879/53

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profile of at least one gene in a peripheral blood sample of a patient to at least one reference expression profile of the at least one gene, where the gene patient has a solid tumour, and each of the gene is differentially expressed in peripheral blood monouclear cells (FBMGs) of a first class of patients as compared to PBMGs of a second class of patients have the solid tumour, and each of the first and second classes is a subcluster formed by an unsupervised clustering analysis of gene expression profiles in PBMCs of a population of patients who have the solid tumour, and where the majority of the first class of patients has a first clinical outcome, the majority of the second class of patients has a second clinical outcome. Also described are: a system comprising (i) a memory or a storage medium including data that represent an expression profile of a curron of patients has a first class a solid tumour, (ii) at least one reference expression profile of the gene, (iii) at least one reference expression profile of the gene, (iii) at represent at least one reference expression profile of the gene, (iii) at program, where expression levels of the gene in peripheral blood tumour calls of patients who have the solid tumour correlate with clinical outcomes of the patients, and an uncleic acid or protein array comprising concentrated probes for solid tumour prognosis genes, where each of the second class of patients as compared to PBMCs of a second class of patients as compared to PBMCs of a second class of patients as compared to PBMCs of a second class of patients as compared to PBMCs of a second class of patients as solid tumour prognosis gene of the invention. Note: The sequence data for this patent did not form at the brinted specification, but was obtained in electronic format.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 526 BP; 111 A; 83 C; 129 G; 57 T; 0 U; 146 Other;
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ö Gaps 635 ö Length 526; 100.0%; Pred. No. 5.2e-08; iive 0; Mismatches 0; Indels Score 50; DB 13; 2.7%; Best Local Similarity 100. Matches 50; Conservative Query Match RESULT 10 AAS25051 ઠે 원

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Human ovarian PCR-subtracted cDNA library clone #1232.
AAS25051 standard; cDNA; 580 BP
                 (first entry)
                                            primer; probe.
                 07-NOV-2001
        AAS25051;
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Immunogenic protein; cancer; ovarian tumour; T-cell stimulation; ss; gene therapy; cytostatic; T-cell expansion; nucleic acid hybridisation; Homo sapiens.

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04-FEB-2000; 2000US-0180403P
                                                                                                                                                       28-MAR-2000; 2000US-0192745P.
                                                                                       05-FEB-2001; 2001WO-US003733
                                                                                                                                                                                                      (CORI-) CORIXA CORP.
WO200157207-A2
                                            09-AUG-2001.
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Algate PA, Mannion J;

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                                                                                                                                         The invention comprises compositions used for the therapy and diagnosis of ovarian cancer. The compositions comprise one or more ovarian tumour proteins, their associated polynucleotides, or immunogenic portions of the proteins. The ovarian tumour polynucleotides and polypeptides are useful for stimulating and/or expanding T cells specific for a tumour protein. They are also useful for inhibiting the development of cancer in a patient with an ovarian tumour DNA or protein by incubating isolated T-cells allowing them to proliferate, and administering to the patient. The sequences can be used as markers for cancer, for example, to monitor ovarian cancer progression. Probes and primers are useful in nucleic acid hybridisation, in detecting the presence of complementary sequences in a given sample, for preparing mutant species and for preparing other genetic constructions. Sequences AAS23820-AAS25231 and AAS25328-AAS25549
                               New polynuclectides encoding ovarian tumor proteins, useful for treating ovarian cancer, and as probes, primers, and markers of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human ovarian tumour associated polynucleotide sequence SEQ ID NO:1320.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAH82377 to AAH83878 represent human ovarian tumour-associated polynucleotide sequences which encode ovarian tumour proteins. The ovarian tumour proteins and polynucleotide sequences have cytostatic activity, and can be used in gene therapy and vaccine production. The ovarian tumour proteins and polynucleotides can be used to inhibit the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel ovarian tumor proteins, and nucleic acids encoding them, used to treat and diagnose cancers, particularly ovarian cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 580 BP; 155 A; 136 C; 172 G; 108 T; 0 U; 9 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 580;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                              represent human ovarian tumour protein cDNA clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 50; DB 4; Le
Pred. No. 5.1e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 2.7%; Score 50; DB Best Local Similarity 100.0%; Pred. No. 5.1 Matches 50; Conservative 0; Mismatches
                                                                                                            Example 1; Page 301-302; 378pp; English.
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                                                                        progression.
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WPI; 2004-269571/25.
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26-SEP-2002;
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MB.
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                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                            578
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                                                                                                                                                                                                                                                                                                                                                                      Matches
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development of cancer, particularly ovarian cancer. They can also be used to diagnose the onset and progression of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                              immunomodulator; cytostatic; nootropic; neuroprotective;
antiparkinsonian; antilipaemic; gene therapy; metabolic disorder;
diabetes; obesity; infection; cachexia; cancer; dyslipidaemia;
neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
immune disorder; haematopoietic disorder; gene; ds.
                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alsobrook JP, Anderson DW, Boldog FL, Burgess CE, Catterton E; Edinger SR, Ellerman K, Gerlach VL, Gorman L, Guo X, Ji W; Kekuda K, Leach MD, Li L, Miller CE, Patturajan M, Rieger DK; Rochenberg ME, Shimkers RA, Smithson G, Spytek KA, Taupier RJ; Vernet CAM, Voss EZ, Zerhusen BD, Zhong M;
                                                                                                                                                          635
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                                                                                                                                                                                                                                                                                                                                                                                                                             Human; NOV; antidiabetic; anorectic; antibacterial; virucide;
                                                                                                                                                          Sequence 580 BP; 155 A; 136 C; 172 G; 108 T; 0 U; 9 Other;
                                                                                    2.7%; Score 50; DB 5; Length 580;
.00.0%; Pred. No. 5.1e-08;
                                                                                                                       0; Indels
                                                                                             100.0%; Pred. w.
                                                                                                                                                                                                                                                                                                                                                                                            Human NOV16e coding sequence.
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2001US-0327917P.
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2001US-0328044P.
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2001US-0328849P.
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                                                                                                                       50; Conservative
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P-PSDB; ABR58397.
                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2003029423-A2.
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12-OCT-2001; 2
15-OCT-2001; 2
17-OCT-2001; 2
22-OCT-2001; 2
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24-OCT-2001;
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01-NOV-2001;
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17-APR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-OCT-2002;
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                                                                                                                                                                                                                                                                                                                      ACC72109;
                                                                                    Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NTRAN, neurotransmission-associated protein, cytostatic; antiarteriosclerotic; anti-HIV; antiallergic; cerebroprotective; antiantiantipartismonian; anticonvulsant; dermatological; nootropic; neuroprotective; antialfammacory; antithyroid; antiarthritic; anorectic; cardiant; hypotensive; hepatotropic; gene therapy; human; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sprague WW;
Becha SD, Khare R;
Marquis JP, Swarnakar A;
         ö
         preventing
NOVX polypeptides and nucleic acids useful for diagnosing, preventing treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 901;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 901 BP; 221 A; 236 C; 292 G; 152 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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100.0%; Pred. No. 4.7e-08;
tive 0; Mismatches 0;
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                                                                                                                                                 Claim 20; Page 155-156; 487pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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/*tag= a
/product= "NTRAN"
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2002US-04087B1P.
2002US-0414221P.
2002US-0426483P.
2002US-0431566P.
2002US-04317P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADM72164 standard; cDNA; 934
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                 pharmacogenomics.
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expressed by standard recombinant methodology. The polypeptides can be expressed by standard recombinant methodology. The polypeptides and polymucleotides are useful in diagnosing, preventing or treating diseases or conditions associated with the decreased expression or overexpression of NTRAN, such as autoimmune/inflammatory, cardiovascular, neurological, developmental, cell proliferative, transport, psychiatric, metabolic or endocrine disorders. These diseases may include AIDS, allergies, atopic dermatitis, arthritis, thyroiditis, obesity, Parkinson's disease, hypertension, cancer, atherosclerosis or hepatitis. These are also useful in assessing the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of NTRAN. The NTRAN or its nucleic acid and amino acid sequences of NTRAN. The NTRAN or its cragments are useful in screening compounds for effectiveness as agonist or an agonist of the polypeptides, or in altering the expression of the transport of the polypeptide, or in altering the expression of the transport of the polypeptide. The microarray is useful in monitoring or measuring protein-protein interactions, drug-target interactions, and expression profiles. The present sequence represents a specific
                               New human neurotransmission-associated proteins and polynucleotides for diagnosing, preventing or treating diseases or conditions associated with aberrant protein expression, e.g. cancer, hepatitis, AIDS, obesity or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; gene; ss; immunological response; immunopathological condition; Crohn's disease; asthma; ulcerative colitis; hypereosinophilia; irritable bowel syndrome; osteoarthritis; rheumatoid arthritis; acute monocytic leukaemia; antiinflammatory; antiaethmatic; antiulcer;
                                                                                                                                                                     The invention relates to human neurotransmission-associated proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     example of a polynucleotide encoding a human NTRAN polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 934 BP; 232 A; 248 C; 283 G; 171 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.7%; Score 50; DB 12; L
100.0%; Pred. No. 4.7e-08;
ative 0; Mismatches 0;
                                                                                                                                 Claim 5; SEQ ID NO 45; 216pp; English
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P-PSDB; ADM72134
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                                                                                               stroke.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Gaps

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comprising obcaining nucleic acids from a sample, confeacing the nucleic acids of the sample with an array comprising the plurality of CDNAs under conditions to form one or more hybridisation complexes, detecting the hybridisation complexes and comparing the levels of the detected conditions to complexes with the level of hybridisation complexes with the level of hybridisation complexes or complexes or complexes correlates with the presence of an hybridisation complexes correlates with the presence of an immunopathological condition. Also disclosed are an expression profile comprising a microarray and a plurality of detectable complexes and a comprising a microarray and a plurality of polynucleotide probes. The CDNAs are useful as hybridisable array elements in a microarray can be used in the expression of target polynucleotides. The microarray can be used in the diagnosis of an immunopathology, such as Crohn's disease, asthma, collecative colitis, hypereosinophilia, irritable bowel syndrome, costeoarthritis, rheumatoid arthritis or acute monocytic leukaemia, and in carcinogenicity studies, for the treatment of the diseases. The microarray may also be used in drud discovery and development, toxicological and carcinogenicity studies, forensics or pharmacogenomics. The composition companies of the printed specification of a subpopulation of mRNAs, cDNAs or genomic fragments. This sequence represents a human cDNA of the invention. Note: The sequence data for this patent did not form part of fram Inspection of the printed specification but was obtained in electronic format directly fram Inspection of the printed specification but was obtained and electronic format directly format directly format missed in pure manners.
                                                                                                                                                    The invention relates to a composition comprising a plurality of cDNAs for detecting the altered expression of genes in an immunological response. The invention also relates to a method of diagnosing or monitoring the treatment of an immunopathological condition in a sample, comprising obtaining nucleic acids from a sample, contacting the nucleic
       altered expression of genes in an immunological response or for diagnosing and treating an immunopathology, e.g. Crohn's disease, asthma or osteoarthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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comprising a plurality of cDNAs, useful for detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               635
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Pred. No. 4.5e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.7%; Scort. No. *...
v 100.0%; Pred. No. *...
i... 0; Mismatches
                                                                                                              Claim 1; SEQ ID NO 140; 50pp; English.
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nes 50; Conservative
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Matches
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The invention relates to polynucleotides which are used as probes to detect genes differentially expressed in an immunological response, abundantly expressed in an immunological response, polypeptide known to regulate blood cell biology. The polynucleotides are useful in research and diagnostic applications particularly in cancer and immunopathological conditions, such as AIDS, allergies, ansemia, asthma, atherosclerosis, bronchitis, ulcerative colitis, diabetes, multiple sclerosis, osteoporosis, pancreatits, infections and arthritis. The present sequence represents a human lymph node cDNA used to detect blood cell and immunological response gene expression. Note: The present sequence does not appear in the printed specification but was obtained in electronic format from the USPTO web site (seqdata.uspto.gov/sequence.html?DocID=2004003).
                                                                      New compositions having a number of first, second and third polynucleotide probes, useful in research and diagnostic applications in cancer and immunological conditions e.g. AIDS, diabetes, osteoporosis and infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1201 BP; 293 A; 342 C; 347 G; 219 T; 0 U; 0 Other;
                                                                                                                                                                                                                 Claim 15; SEQ ID NO 140; 16pp; English.
Seilhamer JJ;
  Stuart SG,
                                             WPI; 2004-387937/36.
  Cocks BG,
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Gaps ö Length 1201; 0; Indels Query Match
2.7%; Score 50; DB 13; L
Best Local Similarity 100.0%; Pred. No. 4.5e-08;
Matches 50; Conservative 0; Mismatches 0; ሯ

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K0143E06-E0433C02-

MNS31093 AGENCOURT BB661026

BB504341 BB190512

602873203 AGENCOURT BB605812 BB498921

CF732471 BBS 04341 BBS 04341 BBS 04341 BBS 0512275 CCX217093 CCX217093 CCX217093 CCX217093 CCX217093 CCX217093 BBF 0192 BBF 08521 BBF 08523 BBF 08

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AK086940 11987 bp mRNA linear HTC 03-APR-2004 Mus musculus 0 day neonate lung cDNA, RIKEN full-length enriched library, clone:B030013502 product:1600055D17RIK PROTEIN (PUTATIVE RETINOIC ACID-REGULATED PROTEIN) (RIKEN CDNA 1600025D17 GENE), full
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
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Nature 409, 685-690 (2001)
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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The FANTOM Consortium and the RIKEN Genome Exploration Research Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Lastor 420, 563-573 (2002)

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Please visit our web site for further details.
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Adachi, J., Alzawa, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Fukuda, S., Furuno, M., Hianagaki, T., Hara, A., Hashizume, W., Fukuda, S., Furuno, M., Hiranako, T., Hiranako, T., Hiranako, T., Haranako, T., Haranako, T., Haranako, T., Haranako, T., Kojima, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kaya, S., Konno, H., Kantaka, T., Miyazaki, M., Muranaka, M., Nishi, K., Saito, R., Numazaki, R., Ohno, M., Ohasto, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Takaku-Akahira, S., Takada, J., Shibata, K., Shinaki, T., Easaki, T., Eagami, M., Togawa, A., Takahashi, F., Takaku-Akahira, S., Takada, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Direct Submission Hayashizaki, Y. Toyaru, A., Toya, T., Yasunishi, A., Direct Submission Research Group, RIKEN Genomic Science Center (GSC), RIKEN Yokohama Institute; 11-722 Suchiro-cho, Tsurumi-ku, Yokohama, Shonasia and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Science Center (GSC), Fax: 81-45-503-9216)

Fax: 81-45-503-9216)

Full Library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group Broyler and Chence Encyclopedia Project of Genome Exploration Research Group Division of Experimental Animal Research in Riken contributed to
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db_xref="GI:26340088"
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Pujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format Genome Res. 10 (11), 1757-1771 (2000)
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
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Please visit our web site for further details.
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MUS mUSCULUS ES cells cDNA, RIKEN full-length enriched library,
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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1029 CAACAGCAAAAAAAACAAAAAACAAAAAAAAAAAAAAA	RESULT 3 AK031742 LOCUS Mus musculus 11 days embryo head cDNA, RIKEN full-length enriched library, clone:6230400B22 product:1600025D17RIK PROTEIN (PUTATIVE RETINOIC ACID-REGULATED PROTEIN) (RIKEN CDNA 1600025D17 GENE), full insert sequence. ACCESSION AK031742 AK031742 AK031742. GI:26327580 KEYWORDS MUS musculus (house mouse) ORGANISM musculus (house mouse) SCUNCE ORGANISM musculus (house mouse) SCURCE ORGANISM musculus (house mouse) SCURCE ALMARADA, GIARAZOA, Chordata, Craniata, Vertebrata; Euteleostomi; Musmalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi, Muridae; Musinae; Mus. AUTHORS A
Questy Match 91.94* Sect. No. 0, Dec. 10.00 91.94* Dec. 10.00 90.00 91.94* Dec. 10.00 90.00 </td <td>Qy 729 ATCCAAGAAGAGCGCAGCGGAGTCAAGGGCTCCTCCAGTGGCAGCAGCAAGCA</td>	Qy 729 ATCCAAGAAGAGCGCAGCGGAGTCAAGGGCTCCTCCAGTGGCAGCAGCAAGCA

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KEVIDTGYGILDGKGSGVKYTKSDLRLIEVTETICKRLLDYSLHKERTGSNRFAKGMS
SPETLHNYHVYKGVKVWDIPTELWERSASVADLKKQCDVLVBEFBEVIEDWYRNHQ
BEDLTBFLCANHVLKGKDYSCLABEWSGKKGDIASLGGKKSKKKRSGVKGSSSGSSKQ
RKELGGLGEDANAEREEGVQKASPLPHSPPDEL"
                                                                                                                                                                      translation="PAPKLGPSPAGAEETDWVRLPSKCEVCKYVAVELKSAFEETGKT
1600025D17 GENE) (SPTR|Q9DAU1, evidence: FASTY, 100%ID,
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                                     Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome_Res. 10 (10), 1617-1630 (2000)
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Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

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Functional annotation of a full-length mouse cDNA collection
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/db_xref="taxon:10090"
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/tissue type="kidney"
/clone_lib="RIKEN full-length er
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72. .902
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Division of Experimental Animal Research in Riken contributed
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/db xref="GI:12838153"
                                                                                                                                                                                                                                                                        organism="Mus musculus"
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                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Warahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-1384-format Genome Res. 10 (11), 1757-1771 (2000)
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     Mus musculus adult female placenta cDNA, RIKEN full-length enriched library, clone:1600025D17 product:1600025D17RIK PROTEIN (PUTATIVE RETINOIC ACID-REGULATED PROTEIN) (RIKEN CDNA 1600025D17 GENE), full
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length CDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 1553)
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Sciurognathi, Muridae, Murinae, Mus.
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Encyclopedia Project of Genome Exploration Research Group in Ri
Genomic Sciences Center and Genome Science Laboratory in RIKEN
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AKO82749 1376 bp mRNA linear HTC 03-APR-2004 Mus musculus ES cells cDNA, RIKEN full-length enriched library, clone:C330002N05 product:1600025D17RIK PROTEIN (PUTATIVE RETINOIC ACID-REGULATED PROTEIN) (RIKEN CDNA 1600025D17 GENE), full insert
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Mus musculus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
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    Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
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                                                                                                                                                       'organism="Mus musculus"
                                                                                                                                                                    /mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                      Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishli, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases I to 1376)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the RIKEN Genome Exploration Research Group Phase II Team and the
                                                                                                                                                                                                        Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected CDNAs to prepare full-length CDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
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Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
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URL:http://fantome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
                                                                                                         cloning
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/db_xref="taxon:10090"
                                                                      Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA
Meth. Enzymol. 303, 19-44 (1999)
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/strain="C57BL/6J"
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The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Adalysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

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Rachaya, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y.,

Ruruno, M., Hanagaki, T., Hara, A., Hayateu, N., Hiramoto, K.,

Hiraokar, T., Horl, F., Imotani, K., Ishii, Y., Itoh, M., Isawa, M.,

Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M.,

Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K.,

Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C.,

Saito, H., Saito, P., Sakai, C., Sakai, K., Sano, H., Soaski, D.,

Shibata, K., Shibata, Y., Shibata, Y., Shiraki, T., Sogabe, Y.,

Shibata, K., Shibata, Y., Shimagawa, A., Takahashi, F., Tanaka, T.,

Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K.,

Yoshino, M., Muramatsu, M. and Hayashizaki, Y. Toshida, K.,

Submitted (10-ULD-200) Yoshinide Hayashizaki, The Institute of

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Kanagawa 230-0045, Japan (E-mail:genome-reseascriken.jp,

WEL:http://genome-gsc.riken.jp/, Tel:81-45-503-9222,

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Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGATCCAAGAGCTCTTTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGTTAATTAAATTAAATCCCCCCCCCCC 3']. cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: XhoI; 3' end: SstI.
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/clone lib="RIKEN full-length enriched mouse cDNA library"
225. .1217
Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system-384-format Genome_Res. 10 (11), 1757-1771 (2000)
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ACID-REGULATED PROTEIN) (RIKEN CDNA 1600025D17 GENE)
(SPTR|Q9DAU1, evidence: FASTY, 100%ID, 100%length,
                                                                                                                                                                                                                                                                                                                                                                       FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
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/mol_type="mRNA"
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Seet Local Similarity 99.4%; Pred. No. 0; No. 0; Matches 1341; Conservative 0; Mismatches 7; Indels 1; Gaps 443 TTGAGACGCTGACAACCTAGTCCACAAGGGGTCAAGGTGATGATATCCCTATG 1 1 1 1 1 1 1 1 1	4.78 743 803 803 862 862 858 778 982 778 1102 1102 1222 1222 1222 1222 1262	1342 CAAACTCC 1138 CAAACTCC 1402 AGAGGGGG 1198 AGAGAGGG
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NIH_MGC_258"
r: pExpress-1; Site_1: NotI; Site_2: EcoRV;
from human embryonic stem cells isolated from
il mass of blastocyst stage embryos and
ed to an early endodermal cell type. Cell line
                                                                                                                                                                                AGGAGGTGCTGGGAGCGCCCGGGGTTGGTTTGGGGTAATC 1701
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NIH_MGC_258 Homo sapiens cDNA clone
A sequence.
                                TRGTTCCTGGGTCCTCATCAGCCTCCAGAGTGTCCCCTCAT 1581
                                                                                                      CCCCCAATCCCAGGGGTGGAAGGCCATCACCATCATTGGA 1641
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INGCTCTGCCCAGCCCTTCTCCCAGGGCTACCAGAGTAAAC 1317
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by: The I.M.A.G.B. Consortium (LLNL)
aboratory for Genomics and Bioinformatics,
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f Health, Mammalian Gene Collection (MGC)
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id and NIH Registry designation is BGO1. Positive for GATA4, MixL1, Msx1, HNF4alpha expression; negative for AFP expression. Passage number 40. cDNA primed using oligo-dr primer: 5'-pGACTAGTYCCGGAGCGGCCCC(T)25-3' and cloned into the ECORV/NotI sites of pExpress-1. This primary library is non-normalized (normalized primary library is non-normalized (normalized primary library is NIH_MGC_259). It was constructed by Express Genomics (Frederick, MD). Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA. Note: this is a Mammalian Gene Collection library."
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100.0%; Pred. No. 5.7e-301;
ive 0; Mismatches 0;
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Best Local S:
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                   Ph.D. construction: Life Technologies, Inc. constitution: Library Preparation: Life Technologies, Inc. constitution arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://inage.llnl.gov Plate: LLAM10978 row: o column: 17 High quality sequence stop: 761.
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                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection Unpublished (1999)
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/tissue_type="tumor, gross
/dev_stage="5 months"
/lab_host="DHIOB"
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="NMRI"
                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
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Size selected for the >lkb fragments, average insert size 1.2 kb. Normalization to Cot 7.5. Tissue contributed by David Rowe; library constructed by ResGen, Invitrogen Corp. Note: this is a NIH MGC Library."
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Glires; Rodentia;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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                                                                                                           Length 903
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Pred. No. 1.5e-265;
                                                                                            36.9%; Sco...
100.0%; Pred. No. ...
... 0; Mismatches
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AGENCOURT 8932400 NIH MGC_94 B5', mRNA sequence.
BQ922065
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| organism="Mus musculus"
| organism="Mus musculus"
| mol_type="mRNA"
| db_xref="taxon:10090"
| clone="IMAGE:30288666"
| tissue_type="embryonic limb, maxilla and mandible"
| clone="IMAGE:30288666"
| tissue_type="embryonic limb, maxilla and mandible"
| clone lib="NIH MGC 136"
| clone lib="NIH MGC 136"
| clone lib="vector: pcwv-Sporf6.1; Site 1: EcoRV; Site 2: Not1;
| Normalized, full-length enriched library from pool of mouse embronic limb, maxilla and mandible, embryonic day
| 17.5, 18.5 and newborn (mandible (5, 4 and 1 limb and jaw equivalents from respective days). Cloned directionally, oligo-dT primed (5'-GACTAGTTCTAGATCGCGAGGCGCCC(T)15-3'.
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Sciurognathi; Murcidea; Murinae; Mus.

1 (Dases 1 to 903)

S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Rober Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Dr. David Rowe

cDNA Library Preparation: Invitrogen Corp

CDNA Library Preparation: Invitrogen Corp

CDNA Library Preparation: Invitrogene Corp

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Plate: NDAM326 row: j column: 01

High quality sequence stop: 611.
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                                                                                                                                                                                                                                                                                                                                                                              TGGTAAATTCGAGAACTTCCAGGACAAACTCGGGTGTGGCACAAAGGGGGCTGGACGCCAG 1377
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                                            CAGCAGCCAGGCCTGCTTCCTTCCACCAAGCATTCTCTTCTGCTGCTGGTCCTTGTGAA
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                                                                                                                        AGGGAAGAGGAGGAGCAGCTCTCTTTCTACACAGTCCCCTCACGAGCTC
                                                                                                                                                               CGGGGTCCACCCAGCATCCCCAGGCTGAGATCCAGGCTCCTGACATGGAAGCTGAAGAGC
                                                                                                                                                                                  CGGGGTCCACCCAGCTCCCCAGGCTCAGGATCCAGGCTCCTGACATGGAAGCTGAAGAGC
                                                                                                                                                                                                                                      CAGCAGCCAGGCCTGCCTCTTCCTTCCACCAAGCATTCTCTTCTGCTGGTCCTTGTCGGA
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1. .932

/ Organism="Mus musculus"

/ mol_type="mRNA"

/ db xere="texaon:10900"

/ clone="InMAGE:30519414"

/ lab_host="DH10B (phage-resistant)"

/ clone="Drgan of Corti"

/ lab_host="DH10B (phage-resistant)"

/ clone lib="Organ of Corti"

/ note="Organ: Organ of Corti"

/ note="Organ of Corti"

/ note="Organ: Organ of Corti"

/ note="Organ of Corti"

/ note="Organ of Corti"

/ note have assigned function; 23* have hits in GenBank, but do not have assigned function; 23* have hits in GenBank, but do not have assigned function; 12* are unidentified. Library created in the laboratory of M. Brownstein (NIMH, NIH). A complete library decription can be found at ."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unpunibaned (1929).
Contact: Daniela S. Gerhard, Ph.D.
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Bechara Kachar and Celine Pompeia, NIDCD.
Tissue Procurement: Bechara Kachar and Celine Pompeia, NIDCD cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM590 row: o column: 07
High quality sequence stop; 579.
                                                                                                                                                                                                                                                                                   AGENCOURT 15614073 Organ of Corti Mus musculus cDNA clone IMAGE:30519414 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi, Muroidea, Muridae, Murinae, Mus.

1 (bases 1 to 892)
NIH-MGC http://mgc.nci.nih.gov/.
                                               601 GGTCCACCCAGCATCCCCAGGCTGAGATCCAGGCTCCTGACATGGAAGCTGAAGAGCATG
                       1141 GGTCCACCCAGCATCCCCAGGCTGAGATCCAGGCTCCTGACATGGAGCTGAAGAGAGATG
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Mus musculus
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/mol type="mass" miscurus
/db Xref="taxon:10090"
/clone="lmAGE:646664"
/tissue type="retina"
/lab_host="DH10B (phage-resistant)"
/clone lib="NHH MGC 94"
/clone="lorgan: eye; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NH_MGC Library."
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.W.A.G.E. Consortium/LLNL at:
http://imaga.llnl.go.
Plate: LLAM13996 row: i column: 17
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  NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                       Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                      High quality sequence stop: 632.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 663; Conservative
                                                     Unpublished (1999)
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/dlone="Tweftor: DGWSport6.1; Site 1: EcoRV, Site 2: NotI;

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           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.lln.gov
Plate: NDAMO651 row: k column: 07
High quality sequence stop: 609.
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1 (Bases 1 to 337)
NIH-WGC http://mgc.nci.nih.gov/.
NIH-WGC http://mgc.nci.nih.gov/.
Ontact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Tissue Procurement: Dr. David Rowe CDNA Library Preparation: Invitrogen Corp
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/cell type="Early passage neurosphere"
/cell type="Rarly passage neurosphere"
/clone lib="Mouse Neurosphere Normalized cDNA library"
/note="Organ: Adult brain; Vector: pCMVSport6.0; A cDNA library was constructed in pCMVsport6.0 from RNA isolated from neurospheres of adult male and female mice. Custom normalized cDNA library by Invitrogen/ResGen"
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Williams, C., Wirta, V., Lundeberg, J. and Frisen, J.
Expressed sequence tags of cDNA clones from murine neurospheres
Unpublished (2005)
Contact: Williams, C.
Molecular Biotechnology
Institution of Biotechnology
AlbaNova University Center, KTH-Royal Institute of Technology, 106
P. Stockholm, Sweden
Tel: +46855378332.
Fax: +46855378481
601 AGGCTGAGATCCAGGCTCTTGACATGGAAGCTGAAGAGCATGAGGCACATAAGATGCTCA 660
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                                                                   MNSISBSS Mouse Neurosphere Normalized cDNA library Mus musculus cDNA 5', mkNA sequence.
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99.9%; Pred. No. 2.1e-248;
iive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cecilia.williams@biotech.kth.se
Seq primer: M13REW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:10090"
/sex="MALE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/strain="C57BL/6"
                                                                                                                                                                                                                      Mus musculus (house mouse)
Mus musculus
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KEYWORDS
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AUTHORS
TITLE
JOURNAL
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                                                                                          CATGCTCTGCCCAGCCCTTCTCCCAGGGCTACCAGAGTAAACACCTTTTGGCCTTTCGGT
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Sequence 151342,
Sequence 151343,
Sequence 151405,
Sequence 151406,
Sequence 3999
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Sequence 23380, A
Sequence 141221,
Sequence 151342,
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Sequence 23, Appl
Sequence 132624,
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                                                                                                              December 30, 2005, 04:07:46 ; Search time 355 Seconds (without alignments) 9208.270 Million cell updates/sec
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1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*

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9: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-09-482-274
US-09-499-016-132624
US-09-949-016-132624
US-09-949-016-134320
US-09-949-016-151342
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US-09-949-016-151343
US-09-949-016-151405
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-09-949-016-12006
-09-949-016-17367
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                                                                                                                                                                                                                                                                                                                                  1303057 seqs, 888780828 residues
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Gapop 60.0 , Gapext 60.0
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Perfect score:
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Sequence 2	Sequence 2	Sequence 2	Sequence 5	Sequence 1	Sequence 1	Sequence 1	Sequence 1	Sequence 1	Sequence 1	Sequence 1	Sequence 1	Sequence 1	Sequence 1	Sequence 1	Sequence 1	Sequence 1	Sequence 1	Sequence 1	Sequence 1	Sequence 1
US-08-361-441B-27	US-08-171-385-20	US-08-361-441B-20	US-09-014-969-5	US-09-205-258-127	US-10-004-860-127	US-08-993-228-11	US-07-813-593-1	US-07-977-451-1	US-07-946-507-1	US-08-252-517-1	US-07-906-397A-1	US-08-601-891-1	US-09-021-324-1	US-09-872-136B-1	US-09-919-408A-1	PCT-US92-02750-1	PCT-US92-05401-1	PCT-US92-09893-1	US-09-949-016-14960	US-09-949-016-16308
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24	24	24	24	24	24	24	24	24	24	24	24	24	74	24	24	24	24	24	24	24
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ALIGNMENTS

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MENDUT IN THE OF INVERNATION:

MENDUT ITLE OF INVENTION TO COKE, Benjamin G. APPLICANT: Jeffrey J. Seilhamer TITLE OF INVENTION: SUBJANCE SUBJANCE SUBJANCE STREET: JATE OF INVENTION: EXPRESSION WITHING PRINCE APPLICANT: Jeffrey J. Seilhamer TITLE OF INVENTION: EXPRESSION WITHING DETECTION OF BLOOD CELL GENE TITLE OF INVENTION: EXPRESSION WITHING DATE: APLA ALTO CORRESPONDENCE ADDRESSE: 100 TREET: JAT POFFTER DRIVE STREET: JAT POFFTER DRIVE STREET: JAT POFFTER DRIVE CONNERS OF STREET: JAT POFFTER DRIVE CONNERS: DEAL POFFTER DRIVE CONNERS: DEAL POFFTER DRIVE STREET: JAT POFFTER DRIVE STREET: JAT POFFTER DRIVE CONNERS: DEAL POFFTER DRIVE CONNERS: DEAL POFFTER DRIVE STREET: JAT DRIVE STREET: JAT
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Sequence 27,

Sequence

US-08-361-441B-22 US-08-171-385-27

Sequence

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TYPE: DNA
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                                                                                                                                                                                                                                                       Sequence 274, Application US/09023655
; Sequence 274, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
    APPLICANT: Cocks, Benjamin G.
    APPLICANT: Suean G. Stuart
    APPLICANT: Suean G. Stuart
    TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
    TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
    TITLE OF INVENTION: EXPRESSION
    NUMBER OF SEQUENCES: 1508
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
    STREET: 3174 PORTER DRIVE
    CITY: PALO ALTO
    STRATE: CALIFORNIA
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                                                                                                                          2.7%; Score 50; DB 3; Length 1201;
100.0%; Pred. No. 4.7e-11;
ive 0; Mismatches 0; Indels
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2.0%; Score 36; DB 3; Length 153
Best Local Similarity 100.0%; Pred. No. 2.9e-05;
Matches 36; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Rloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION DATA:
FILING DATE: HEREWITH
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CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J., 071
REFIRENCE/DOCKET NUMBER: 37, 071
REFERENCE/DOCKET NUMBER: 9A-0(
TELEPHONE: (650) 845-0555
TELEPHONE: (650) 845-4166
INFORMATION FOR EGO ID NO: 274:
SEQUENCE CHARACTERISTICS:
LENGTH: 1534 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMMEDIATE SOURCE:
LIBRARY: BRSTNOT07
CLONE: 1298861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                          Best Local Similarity
Matches 50; Conserv
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US-09-023-655-140
                                                                                                                                                                                                                                                       US-09-023-655-274
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                                        Query Match
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US-09-482-273-23/c ; Sequence 23, Application US/09482273 ; Patent No. 6534631

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; Sequence 132624, Application US/09949016
; Patent No. 681239
; GENERAL INFORMATION:
; APPLICANT: VBYTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; FILE REFERENCE: CLOOD1307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR APPLICATION NUMBER: 60/231,768
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOUTHWARE: PERSESQ FOR Windows Version 4.0
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US-09-949-016-15473
US-09-949-016-15473, Application US/09949016
; Sequence 15473, Application US/09949016
; Patent No. 681239
; GENERAL INFORMATION:
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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100.0%; Pred. No. 0.00051;
iive 0; Mismatches 0;
TITLE OF INVENTION: 71 Human Secreted Proteins FILE REFERENCE: P2030P1
CURRENT APPLICATION NUMBER: US/09/482,273
CURRENT FILING DATE: 2000-01-13
EARLIER APPLICATION NUMBER: PCT/US99/15849
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 267
SOFTWARE: PATENTIN VOMBER: 60/092,956
SARLIER FILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 267
SOFTWARE: PATENTIN VOMBER: 60/092,956
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1000.0%; Pred. No. 0.45;
iive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 733 CCACCAGGAGGAAGACCTGACTGAATTCCTCTG 701
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Best Local Similarity 100.
Matches 26, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
CORGANISM: Homo sapiens
US-09-482-273-23
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US-09-949-016-132624
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ORGANISM: Human
US-09-949-016-141221
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; ORGANISM: Human
US-09-949-016-151342
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Sequence 23380, Application US/09949016

Raten No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REPREMENCE: CLOOL 307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR PAPLICATION NUMBER: 60/231,768

PRIOR PLING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR PLING DATE: 2000-10-03

PRIOR PLING DATE: 2000-09-08

NUMBER OF SEO ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 23380
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF PILE REFERENCE: CL001307
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1.4%; Score 25; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 25; Conservative 0; Mismatches 0; Indels
               CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR PRILING DATE: 2000-04-175
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
STOWNER OF SEQ ID NOS: 207012
SOFTWARE: PRESCR FOR WINDOWS VERSION 4.0
SSOFTWARE: PSECS FOR WINDOWS VERSION 4.0
SERVICH: 450395
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US-089-949-016-141221
Sequence 141221, Application US/09949016
Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                        | PEATURE:
| NAME/KEY: misc_feature
| LOCATION: (1)...(450395)
| OTHER INFORMATION: n = A,T,C or G
| US-09-949-016-15473
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-23380
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FARENCE NO. 0812439

FARENCE NO. 0812439

FARENCE NO. 0812439

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

FILE REFERENCE: CLO01307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-0-09-08

NUMBER OF SEQ ID NOS: 207012

SOCTWARE: FRSEESQ for Windows Version 4.0

SEQ ID NO 151342
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Sequence 151343.
Sequence 151349.
Trib of INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,756
PRIOR APPLICATION NUMBER: 60/237,768
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Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 25; Conservative 0; Mismatches
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1.4%; Score 25; DB 3;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 25; Conservative 0; Mismatches
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-30
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-09-08
NUMBER: OF SEQ ID NOS: 207012
SEQ ID NO 141221
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; Sequence 151342, Application US/09949016
; Patent No. 6812339
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TYPE: DNA
ORGANISM: Human
FEATURE:
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US-09-949-016-151405

Sequence 151405, Application US/09949016

Patent No. 681239

GENERAL INFORMATION:

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOOL307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FESTSEQ for Windows Version 4.0

SEQ ID NO 151405
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Sequence 151406, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: 00/0414,

PRIOR FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

NUMBER OF SEQ ID NOS: 207012
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Pred. No. 1.2;
                                                                                                                                                                                                                                                                                                              0; Indels
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PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 601
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1.4%; Scc
Best Local Similarity 100.0%; Pr
Matches 25; Conservative 0;
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Matches 25; Conservative
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US-09-949-016-151406
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; ORGANISM: Human
US-09-949-016-151405
                                                                                                                                                                                                                     US-09-949-016-151343
                                                                                                                                                                       TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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Sequence 3999, Application US/09949016
; Sequence 3999, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
    APPLICANT: VENTER, J. Craig et al.
    TITLE OF INVENTION: POLYMORPHISMS. IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; CURRENT APPLICATION NUMBER: 60/241,755
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207002
; SCFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NOS: 207002
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| Sequence 15158, Application US/09949016
| Sequence 15158, Application US/09949016
| Retent No. 6812339
| GENERAL INFORMATION:
| APPLICANT: VENTER, J. Craig et al. |
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF |
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF |
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF |
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF |
| TITLE OF INVENTION: 2000-04-14 |
| PRIOR PELING DATE: 2000-04-10-20 |
| PRIOR PELING DATE: 2000-10-03 |
| PRIOR PELING DATE: 2000-10-03 |
| PRIOR PELING DATE: 2000-09-08 |
| NUMBER OF SEQ ID NOS: 207012 |
| SEQ ID NO 15158 |
| LENGTH: 9087 |
| LENGT
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100.0%; Pred. No. ...
0; Mismatches
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1.4%; Score 25; DB
Best Local Similarity 100.0%; Pred. No. 1.1
Matches 25; Conservative 0; Mismatches
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Best Local Similarity 100.0
Matches 25; Conservative
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US-09-949-016-15158/c
                                       ; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-151406
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SEQ ID NO 151406
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; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15629
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Sequence 13251, Application US/09949016

Batent No. 681239

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

FILE REPERENCE: CLOOL 1307

CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR PRILING DATE: 2000-04-14

PRIOR PRILING DATE: 2000-10-20

PRIOR PLING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 13251

LENGTARE: DATE: DATE
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Sequence 15629, Application US/09949016

Patent No. 681239

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUWAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUWAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-14-14

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 19601
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1.4%; Score 25; DB 3; Length 11211;
Best Local Similarity 100.0%; Pred. No. 0.93;
Matches 25; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                               1.4%; Score 25; DB 3; Length 9087;
100.0%; Pred. No. 0.95;
tive 0; Mismatches 0; Indels
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; NAME/KEY: misc_feature
; LCCATION: (1)...(9087)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15158
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; LOCATION: (1)...(11211)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13251
                                                                                                                                                                                                                                                  Best Local Similarity 100.0
Matches 25; Conservative
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US-09-949-016-13251
                                                                                                                                                                                                            Query Match
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y, OXGANIDN: Human
US-09-949-016-15629
Query Match
Best Local Similarity 100.0%; Pred. No. 0.89;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 25; Conservative 1839
Oy 1815 AACTGTAAAAAAAAAAAAAAAAA 1839
Db 18157 AACTGTAAAAAAAAAAAAAAAA 18133
Search completed: December 30, 2005, 09:11:04
Job time: 357 secs
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US-10-430-201-4790

Sequence 4790, Application US/10430201

Sequence 4790, Complication US/10430201

Sequence 4790, Complication No. US20040162679A1

GENERAL INFORMATION:

APPLICANT: Li, Linheng

TITLE OF INVENTION: Method for Predicting Gene Potential and Cell Commitment

TITLE OF INTERNE: 40716 (IP-010)

CURRENT APPLICATION NUMBER: US/10/430,201

CURRENT APPLICATION NUMBER: US 60/370,114

PRIOR FILING DATE: 2002-05-03

NUMBER OF SEQ ID NOS: 4879.
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Sequence 4790, Ap
Sequence 33803, A
Sequence 1232, Ap
Sequence 1232, Ap
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1: /cgn2 6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
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US-10-262-839-67

US-10-262-839-67

US-10-128-008-135

US-10-121-049-135

US-10-121-049-135

US-10-121-049-135

US-10-175-746-135

US-10-175-746-135

US-10-175-746-135

US-10-175-746-135

US-10-175-146-135

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Gapop 60.0 , Gapext 60.0
GenCore (c) 1993
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APPLICANT: Li, Linheng
TITLE OF INVENTION: Method for Predicting Gene Potential and Cell Commitment
FILE REPERENCE: 40716 (IP-01)
CURRENT APPLICATION NUMBER: US/10/430,201
CURRENT FILING DATE: 2003-05-05
PRIOR FILING DATE: 2002-05-03
NUMBER OF SEQ ID NOS: 4879
SOFTWARE: Patentin version 3.2
SEQ ID NO 4789
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                                   Sequence 135, Se
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                        Sequence
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Pred. No. 2.9e-39;
0; Mismatches 0; Indels
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US-10-123-262-135

US-10-142-633-135

US-10-141-755-135

US-10-143-032-135

US-10-123-108-135

US-10-123-26-135

US-10-123-26-135

US-10-123-26-135

US-10-124-0928-135

US-10-124-0928-135

US-10-124-0928-135

US-10-124-0928-135

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US-10-127-088-135

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US-10-127-088-135
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; Publication No. US20040162679A1
; GENERAL INFORMATION:
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Best Local Similarity 100.0%; Pr
Matches 100; Conservative 0;
                                       ; TYPE: DNA
; ORGANISM: Mus musculus
US-10-430-201-4789
   US-10-430-201-4789
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### Sequence 1232, Application US/10015219

### Publication No. US20030008299A1

### GENERAL INFORMATION:
### APPLICANT: Algate, Paul A.

### TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

### TITLE OF INVENTION: COMPOSITIONS OF OVARIAN CANCER

### FILE REPERENCE: 21012.1.493C1

### CURRENT APPLICATION NUMBER: US/10/015,219

### CURRENT APPLICATION NUMBER: US/10/015,219

### WUMBER OF SEQ ID NOS: 1739

### SOFTWARE: FastEEQ for Windows Version 4.0

### SEQ ID NO 1232
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2.7%; Score 50; DB 3; Le
Best Local Similarity 100.0%; Pred. No. 3.4e-14;
Matches 50; Conservative 0; Mismatches 0;
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2.7%; Score 50; DB 5; Le
Best Local Similarity 100.0%; Pred. No. 3.4e-14;
Matches 50; Conservative 0; Mismatches 0;
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GENERAL INFORMATION:
APPLICANT: Alsobrook, John,
APPLICANT: Anderson, David W.,
APPLICANT: Boldog, Ferenc,
APPLICANT: Burgess, Catherine,
APPLICANT: Edinger, Shlomit,
; OTHER INFORMATION: n = A,T,C or G
US-09-777-564-1232
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Taupier, Raymond, jr.,
Vernet, Corine,
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Shimkets, Richard,
Smithson, Glennda,
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Reiger, Daniel,
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Gerlach, Valerie,
Gorman, Linda,
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Miller, Charles,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 580
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APPLICANT:
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APPLICANT:
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Publication No. US20040031072A1

GENERAL INFORMATION:
APPLICANT:
APPLICANT:
CAO YONGWEI
TITLE OF INVENTION:
FILE OF INVENTION:
FILE SEFRENCE:
APPLICANT:
FILE OF INVENTION:
FILE OF INVENTION:
CURRENT APPLICATION NUMBER:
US/10/424,599
CURRENT FILING DATE:
2003-04-28
NUMBER OF SEQ ID NOS:
285684

EENGTH: 444
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                                                                                                                                                                                             Gaps
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; Batent No. US2002022591A1
; GENERAL INFORMATION:
; APPLICANT: Algate, Paul A.
; APPLICANT: Algate, Paul A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.49
; CURRENT FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 1730
; SEQ ID NO 1232
; LENGTH: 580
; LENGTH: 580
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2.7%; Score 50; DB 7; Length 444;
Best Local Similarity 100.0%; Pred. No. 3.5e-14;
Matches 50; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                       514 GAGACCTCAGCAGAGGTGGCTGACCTCAAGAAGCAGTGTG 553
                                                                                                                                                                                                                                                                                                                                                              61 GAGACCTCAGCAGAGGTGGCTGACCTCAAGAAGCAGTGTG 100
                                                                                                                                                 Query Match 5.4%; Score 100; DB 7; Lo
Best Local Similarity 100.0%; Pred. No. 2.9e-39;
Matches 100; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Clone ID: PAT_MRT3847_130528C.1
US-10-424-599-33803
  SOFTWARE: PatentIn version 3.2
SEQ ID NO 4790
LENGTH: 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(580)
                                                                 ) TYPE: DNA
, ORGANISM: Mus musculus
US-10-430-201-4790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Glycine max
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US-09-777-564-1232
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APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLECTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-KB PATHWA
FILE REPERENCE: D01004.np
CURRENT APPLICATION NUMBER: US/10/126,103
CURRENT APPLICATION NUMBER: US 60/284,962
PRIOR APPLICATION NUMBER: US 60/284,962
PRIOR PILING DATE: 2001-04-19
PRIOR APPLICATION NUMBER: US 60/286,645
PRIOR APPLICATION NUMBER: US 60/346,986
PRIOR FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 284
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TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-KB
TITLE OF INVENTION: PATHWAY
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Pred. No. 3.1e-14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE DESCRIPTION: SEQ ID NO: 140 : US-10-641-643-140
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     PRIOR APPLICATION DATA:
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET VUMBER: PA.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 139, Application US/10431096
Publication No. US20040086896A1
GENERAL INFORMATION:
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Publication No. US20030224486A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.7%; Sco..
100.0%; Pre
                                                                                                                                                                                                                                                       845-4166
                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1201 base pairs
                                                                                                                                                                                                                                                       TELEFAX: (650) 845-41
INFORMATION FOR SEQ ID NO: 140:
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SEQ ID NO 139
LENGTH: 1378
                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: singl
                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear IMMEDIATE SOURCE: LIBRARY: THPINOB01
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Best Local Similarity 100.0
Matches 50; Conservative
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US-10-126-103-139
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Best Local Similarity
Matches 50; Conserv
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APPLICANT: Zhong, Mei
TITLE OF INVENTION: THERABEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOL
FILE REFERENCE: 21402-4628
CURRENT APPLICATION NUMBER: 06/326,483
PRIOR PELICATION NUMBER: 60/326,483
PRIOR APPLICATION NUMBER: 60/326,483
PRIOR APPLICATION NUMBER: 60/327,917
PRIOR APPLICATION NUMBER: 60/328,029
PRIOR APPLICATION NUMBER: 60/328,029
PRIOR PELING DATE: 2001-10-09
PRIOR PELING DATE: 2001-10-09
PRIOR PELING DATE: 2002-69-16
PRIOR APPLICATION NUMBER: 60/321,101
PRIOR APPLICATION NUMBER: 60/321,101
PRIOR APPLICATION NUMBER: 60/321,342
PRIOR APPLICATION NUMBER: 60/321,342
PRIOR PELING DATE: 2002-10-05
PRIOR PELING DATE: 2001-10-05
PRIOR PELING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 60/328,044
PRIOR PELING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 60/328,444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.7%; Score 50; DB 7; Length 901; 100.0%; Pred. No. 3.3e-14; trive 0; Mismatches 0; Indels
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CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/10/641,643 PILLING DATE: 14-Aug-2003
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Publication No. USZ0040077003A1
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
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COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
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Best Local Similarity
Matches 50; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LOCATION: (47)..(880)
US-10-262-839-69
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US-10-641-643-140
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SEQ ID NO 69
LENGTH: 901
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Gaps
                          PRIOR FILING DATE: 2002-04-12
PRIOR APPLICATION NUMBER: 60/327,342
PRIOR FILING DATE: 2001-10-05
PRIOR FILING DATE: 2001-10-05
PRIOR FILING DATE: 2001-10-09
PRIOR FILING DATE: 2001-10-09
PRIOR FILING DATE: 2001-10-12
PRIOR FILING DATE: 2001-0-12
PRIOR FILING DATE: 2002-04-23
REMAINING PRIOR APPLICATION NUMBER: 60/374,738
PRIOR FILING DATE: 2002-04-23
SEQIENCE OF SEQIENCE OF SEQUENCE OF PALM.
NUMBER OF SEQIENCE VERSION 0.1
SEQIENCE OF SEQUENCE OF 
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100.0%; Pred. No. 3.1e-14;
tive 0; Mismatches 0;
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CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/049911
PRIOR APPLICATION NUMBER: 60/049911
PRIOR PLING DATE: 1997-06-18
PRIOR PLING DATE: 1997-08-26
PRIOR PLING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059113
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR PLING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/05912
PRIOR APPLICATION NUMBER: 60/05912
PRIOR APPLICATION NUMBER: 60/05912
PRIOR PLING DATE: 1997-09-17
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Publication No. US20030004311A1
GENERAL INFORMATION:
APPLICATION NUMBER: 60/371,972
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Stewart, Timothy A.
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Wood, William
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Filvaroff, Ellen
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Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sherwood, Steven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 50; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumas, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; NAME/KEY: CDS
; LOCATION: (388)..(549)
US-10-262-839-67
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TITLE OF INVENTION:
FILE REFERENCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1596
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APPLICANT:
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APPLICANT: Zerhusen, Brian,
APPLICANT: Zhong, Mei
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
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2.7%; Score 50; DB 7; Length 1378;
Best Local Similarity 100.0%; Pred. No. 3.1e-14;
Matches 50; Conservative 0; Mismatches 0; Indels
                          CURRENT APPLICATION NUMBER: US/10/431,096
CURRENT FILING DATE: 2003-05-07
PRIOR APPLICATION NUMBER: US 60/284,962
PRIOR FILING DATE: 2001-04-19
PRIOR PILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: US 60/286,645
PRIOR PILING DATE: 2002-04-19
PRIOR FILING DATE: 2001-04-26
PRIOR FILING DATE: 2001-04-26
PRIOR FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 307
SOFTWARE: PERCENTIN VERSION 3.2
LENGTH: 1378
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CURRENT APPLICATION NUMBER: US/10/262,839
CURRENT FILING DATE: 2002-10-01
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R FILING DATE: 2001-10-09
R PILING DATE: 2001-10-09
R PILING DATE: 2001-10-09
RR APPLICATION NUMBER: 60/381,101
R FILING DATE: 2002-05-16
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PRIOR APPLICATION NUMBER: 60/326,483
PRIOR FILING DATE: 2001-10-02
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FILING DATE: 2001-10-09
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Publication No. US20040038877A1
GENERAL INFORMATION:
APPLICANT: Alsobrook, John,
APPLICANT: Anderson, David W.,
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Vernet, Corine,
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Burgess, Catherine,
Catterton, Elina,
Edinger, Shlomit,
Ellerman, Karen,
Gerlach, Valerie,
Gorman, Linda,
Goo, Xiaojia,
Ji, Waizhen,
Kekuda, Ramesh,
Leach, Martin,
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Reiger, Daniel,
Rothenberg, Mark,
Shimkets, Richard,
Smithson, Glennda,
Spytek, Kimberly,
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Miller, Charles,
      REFERENCE: D0108A CIP
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; ORGANISM: Homo sapiens
US-10-431-096-139
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US-10-262-839-67
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NUMBER: 60/059352 1997-09-19 NUMBER: 60/05988 1997-09-19 NUMBER: 60/06250 1997-10-17 NUMBER: 60/062250 1997-10-17 NUMBER: 60/062285 1997-10-17 1997-10-17 NUMBER: 60/06281 1997-10-17 NUMBER: 60/06281 1997-10-17	NUMBER: 60/06281. 1997-10-24 1097-10-24 11997-10-24 11997-10-31 11997-10-31 11997-10-31 11997-10-31 11997-10-37 11997-10-37 11997-10-37 11997-10-38 11997-10-38 11997-10-38 11997-10-38 11997-10-38 11997-10-38 11997-10-38 11997-10-39	NUMBER: 60/065846 1997-11-17 NUMBER: 60/066453 1997-11-24 NUMBER: 60/066511 1997-11-24 NUMBER: 60/066511 1997-11-24 NUMBER: 60/06912 1997-12-11 NUMBER: 60/069278 1997-12-11 NUMBER: 60/069278 1997-12-11 NUMBER: 60/06934 1997-12-11 NUMBER: 60/06934 1997-12-12 NUMBER: 60/073120 1998-02-04 NUMBER: 60/073120 1998-02-04 NUMBER: 60/073120 1998-02-09 NUMBER: 60/073121 NUMBER: 60/073121 NUMBER: 60/073121 NUMBER: 60/073121 NUMBER: 60/073121 1998-02-09 NUMBER: 60/073121
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PRIOR FILING DATE: 1998-03-12
PRIOR PRICATION UNDERS: 60/07924
PRIOR APPLICATION NUMBER: 60/07924
PRIOR PLILICATION NUMBER: 60/07924
PRIOR PLILICATION NUMBER: 60/07928
PRIOR PLICATION NUMBER: 60/07928
PRIOR PLICATION NUMBER: 60/09129
PRIOR PLICATION NUMBER: 60/09139
PRIOR PLICATION NUMBER: 60/09130
PRIOR PLICATION NUMBER: 60/091

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Stewart, Timothy A
                                                                                                             Gerritsen, Mary E.
                                                       Desnoyers, Luc
Filvaroff, Ellen
                                                                                                                                               Godowski, Paul J. Gurney, Austin L.
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                                                                                                                                Goddard, Audrey
                                                                                          Gao, Wei-Qiang
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APPLICANT:
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APPLICANT:
APPLICANT:
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APPLICANT:
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P33330R1C182
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                                                                                                                                                                                                                                                                              DB 5; Length 1675; 3.1e-14;
                                                                                                                                                                                                                                                                                                                  0; Indels
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CURRENT FILING DATE: 2002-05-07
Prior Apploication removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 155
LENGTH: 1675
                                                                                                                                                                                                                                                                              2.7%; Score 50; DB 100.0%; Pred. No. 3.1 Live 0; Mismatches
PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-24
PRIOR PELING DATE: 1998-06-24
PRIOR PELING DATE: 1998-06-24
PRIOR PELING DATE: 1998-06-26
PRIOR PELING DATE: 1998-06-26
PRIOR PELING DATE: 1998-06-26
PRIOR PAPLICATION NUMBER: 60/091863
PRIOR PELING DATE: 1998-07-01
PRIOR PELING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR APPLICATION NUMBER: 60/091519
PRIOR APPLICATION NUMBER: 60/09161
PRIOR PELING DATE: 1998-07-01
PRIOR PELING DATE: 1998-07-02
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Publication No. US20030017563A1
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Smith, Victoria
Stewart, Timothy A.
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Goddard, Audrey
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Wood, William
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Gurney, Austin L.
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Filvaroff, Ellen
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Matches 50; Conservative
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Best Local Similarity 100.(
Matches 50; Conservative
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ORGANISM: Homo Sapien
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US-10-121-049-135
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Sequence 135, Application US/10121049 Publication No. US20030022239A1 GENERAL INFORMATION:

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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330RIL17
CURRENT APPLICATION NUMBER: US/10/121,049
CURRENT FILING DATE: 2002-04-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: 93330R1C54 CURRENT APPLICATION NUMBER: US/10/123,904 CURRENT FILING DATE: 2002-04-16
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NUMBER OF SEQ ID NOS: 550
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 135
LENGTH: 1675
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100.0%; Pred. No. 3.1e-14;
tive 0; Mismatches 0;
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Publication No. US20030022328A1
GENERAL INFORMATION:
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Stewart, Timothy A.
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Gerritsen, Mary E.
Goddard, Audrey
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Tumas, Daniel
Watanabe, Colin K
Wood, William
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Gurney, Austin L.
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Filvaroff, Ellen
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CORGANISM: Homo Sapien
US-10-123-904-135
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Best Local Similarity
Matches 50; Conserv
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SECRETED SECONDING THE SAME
PILE REFERENCE: P3330R1C160
CURRENT APPLICATION NUMBER: US/10/140,470
CURRENT PILING DATE: 2002-05-06
PRIOR APPLICATION TEMOVED - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
LENGTH: 1675
                                           0; Gaps
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                                                                                                                                                                   RESULT 15
US-10-140-470-135
Sequence 135, Application US/10140470
PUblication No. US2033022331A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
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Filvaroff, Ellen
Gao, Wei-Qiang
Gerritsen, Mary E.
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Watanabe, Colin K
Wood, William
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Godowski, Paul J.
Gurney, Austin L.
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Smith, Victoria
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ORGANISM: Homo Sapien
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Search completed: December 30, 2005, 09:34:20 Job time : 1383 secs

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Sequence 135, App
Sequence 665859,
                                                                                                  ; Search time 299 Seconds
(without alignments)
3224.269 Million cell updates/sec
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Sequence
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1: /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*

2: /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/DSO7_NEW_PUB.seq:*

4: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*

5: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*

6: /cgn2_6/ptodata/1/pubpna/USO10_NEW_PUB.seq:*

7: /cgn2_6/ptodata/1/pubpna/USO11_NEW_PUB.seq:*

8: /cgn2_6/ptodata/1/pubpna/USO11_NEW_PUB.seq:*

9: /cgn2_6/ptodata/1/pubpna/USO11_NEW_PUB.seq:*

10: /cgn2_6/ptodata/1/pubpna/USO11_NEW_PUB.seq:*
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-10-750-18-35528
US-10-750-18-35528
US-11.12-908-55
US-11.12-908-65
US-11.12-908-63
US-11.12-908-63
US-11.12-908-64
US-11.12-908-62
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US-10-750-185-37066
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US-11-112-908-22
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Gapop 60.0 , Gapext 60.0
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seq length: 2000000000
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ALIGNMENTS

APPLICANT: Watanabe, Colin K
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
PILE REFERENCE: P3330R1C128 CURRENT FILING DATE: 2002-04-24
CURRENT FILING DATE: 2002-04-24
PRIOR FULING DATE: 1997-06-18
PRIOR FILING DATE: 1997-06-18
PRIOR FILING DATE: 1997-08-26
PRIOR PELING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059113
PRIOR PELING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR PELING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-18
PRIOR PELING DATE: 1997-09-18 Application US/10131826A o. US20050245730A1 AFFLANCE DATE: 1997-09-10
APPLICATION NUMBER: 60/059352
TIME DATE: 1997-09-19 FILING DATE: 1997-09-19 APPLICATION NUMBER: 60/059588 Smith, Victoria Stewart, Timothy A. Goddard, Audrey Godowski, Paul J. Gurney, Austin L. Sherwood, Steven Desnoyers, Luc Filvaroff, Ellen Gao, Wei-Qiang Tumas, Daniel Sequence 135, Applic Publication No. US20 GENERAL INFORMATION: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT

22, Appl

Sequence

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Gaps
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APPLICANT: MAI GENOMICS, INC.
APPLICANT: DAVIGE Sue K.
APPLICANT: RERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: ROSENFELD, David
APPLICANT: PATTIN, Dennis
TILLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILLE REFERENCE: MAILION-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT APPLICATION NUMBER: US 60/437,482
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR PILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE PLING APPLICATION VERSION 3.1
SEQ ID NO 38459
LENGTH: 1833
                                                                                                                                                                                                                           APPLICANT: MUNICATION:
APPLICANT: MUNICATION:
APPLICANT: DeNISE, Sue K.
APPLICANT: RESER, Richard
APPLICANT: ROSENFELD, David
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: APPLICANT: APALTIN, Dennis
APPLICANT: PANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INPERRING BOVINE TRAITS
FILE REFERENCE: MMI1100-2
CURRENT FILING DATE: 2003-12-31
PRIOR FILING DATE: 2003-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PALENTIN VETSION 3.1
SEQ ID NO 35528
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Pred. No. 0.56;
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Pred. No. 0.55;
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    606 CCAGGAGGAGCCTGACTGAATTC 630
                                             1 ccaggaggaagaccrgacrgaarrc 25
                                                                                                                                                          Sequence 35528, Application US/10750185; Publication No. US20050260603A1; GENERAL INFORMATION:
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; Sequence 38459, Application US/10750185
; Publication No. US20050260603A1
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US-10-750-185-35528
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US-10-750-185-38459
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Best Local Similarity
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US-11-121-849-665860
Sequence 665860, Application US/11121849
Sequence 665860, Application US/11121849
Sequence 665860, Application No. US20050272080A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Microarrays
FILER REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT APPLICATION NUMBER: US/11/121,849
FILER APPLICATION NUMBER: US/11/121,849
FRIOR APPLICATION NUMBER: 0S/567,949
FRIOR APPLICATION NUMBER: 0S/567,949
FRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SEQ ID NO 655860
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded STITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded STITLE OF INVENTION: Microarrays
TITLE OF INVENTION: Microarrays
TITLE STEPERENCE: 564.1
CURRENT APPLICATION NUMBER: US/11/121,849
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
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PRIOR FILING DATE: 1997-09-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 135
LENGTH: 1675
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100.0%; Pred. No. 8.3e-11;
tive 0; Mismatches 0; Indels
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SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 665859
LENGTH: 25
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100.0%; Pred. No.
tive 0; Mismatch
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 665859, Application US/11121849; Publication No. US20050272080A1; GENERAL INFORMATION:
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Matches 50; Conservative
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les 25; Conservative
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US-11-121-849-665860
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CORGANISM: Homo sapien
US-11-121-849-665859
                                                                                                                      TYPE: DNA
ORGANISM: Homo Sapien
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US-11-121-849-665859
                                                                                                                                                       ; OKGRALSH; FICHOUS US-10-131-826A-135
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Best Local Si
Matches 25;
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DENDIGATION NO. US20050266459A1

DENDIGATION NO. US20050266459A1

APPLICANT: POULSEN, TIM S.

APPLICANT: NIELSEN, KIRSTEN V.

TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES FILE REFERENCE: 09138.6000-00000

CURRENT APPLICATION NUMBER: US/11/121,086

CURRENT FILING DATE: 2005-05-04

PRIOR PILING DATE: 2004-05-04

PRIOR FILING DATE: 2004-05-04
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Pred. No. 0.64;
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100.0%; Pred. No. 0.64;
tive 0; Mismatches
APPLICANT: MAITH, COLOR APPLICANT: MAITH, COLOR APPLICANT: Davis, Lisa M.
TITLE OF INVENTION: Breast Cancer Biomarkers
FILE REFERENCE: 04-164-04-12
CURRENT APPLICATION NUMBER: US 60/564,758
PRIOR PLICHING DATE: 2004-04-23
PRIOR PLICHING DATE: 2004-04-23
PRIOR PLILING DATE: 2004-06-01
PRIOR PLILING DATE: 2004-06-01
PRIOR PLILING DATE: 2004-11-30
PRIOR PLILING DATE: 2004-11-30
PRIOR PLILING DATE: 2004-11-07
PRIOR PLILING DATE: 2004-11-07
NUMBER: OF SEQ ID NOS: 511
SOFTWARE: PATENTIN POSE 511
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1.3%; Score 24; DB
Best Local Similarity 100.0%; Pred. No. 0.6
Matches 24; Conservative 0; Mismatches
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APPLICANT: Davis, Lisa M.
TITLE OF INVENTION: Breast Cancer Biomarkers
FILE REFERENCE: 04-164-US
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CURRENT FILING DATE: 2005-04-22
PRIOR APPLICATION NUMBER: US 60/564,758
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 107
SOFTWARE: PatentIn version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0
....hes 24; Conservative
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US-11-112-908-63
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LENGTH: 154548
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US-11-112-908-64/c
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Sequence 665854, Application US/11121849
Sequence 665854, Application US/11121849
Sequence 665854, Application Occupants
Sequence 665854, Application Occupants
Sequence 665854, Application Number of Genetic Analysis of Formalin Fixed Paraffin Embedded (STITLE OF INVENTION: Mctoarrays
TITLE OF INVENTION: Mctoarrays
FILE REFERENCE: 3084.1
CURRENT FILING DATE: 2005-05-03
CURRENT FILING DATE: 2004-05-03
PRIOR FILING DATE: 2004-05-03
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
LENGTH: 25
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                                                                                 Sequence 55, Application US/11112908
Publication No. US20050260659A1
GENERAL INFORMATION:
APPLICANT: Harris, Cole
APPLICANT: Davis, Lisa M.
TITLE OF INVENTION:
FILE FERENCE: 04-164-US
CURRENT APPLICATION NUMBER: US/11/112,908
CURRENT APPLICATION NUMBER: US 60/564,758
PRIOR PILING DATE: 2004-04-23
PRIOR FILING DATE: 2004-04-13
PRIOR PILING DATE: 2004-06-01
PRIOR PILING DATE: 2004-06-01
PRIOR PILING DATE: 2004-11-30
PRIOR PILING DATE: 2004-11-30
PRIOR PILING DATE: 2004-11-30
PRIOR FILING DATE: 2004-12-07
PRIOR FILING DATE: 2004-11-30
PRIOR FILING DATE: 2004-11-30
PRIOR FILING DATE: 2004-11-30
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; Publication No. US20050260659A1
; GENERAL INFORMATION:
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; ORGANISM: Homo sapiens
US-11-112-908-55
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; ORGANISM: Homo sapien
US-11-121-849-665854
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NUMBER OF SEQ ID NOS: 511
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CORGANISM: Homo sapiens
US-11-112-908-65
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US-11-121-086-36
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                                                                                              TYPE: DNA
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APPLICANT: POULSEN, TIM S.
APPLICANT: POULSEN, TIM S.
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES FILE REFERENCE: 09138.6000-00000
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT PILING DATE: 2005-05-04
PRIOR FILING DATE: 2004-05-04
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1.3%; Score 24; DB 7; Length 157230;
Best Local Similarity 100.0%; Pred. No. 0.63;
Matches 24; Conservative 0; Mismatches 0; Indels 0
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; Publication No. US20050260659A1
; GRENERAL INFORMATION:
APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
TITLE OF INVENTION: Breast Cancer Biomarkers
TITLE OF INVENTION: Breast Cancer Biomarkers
; CURRENT APPLICATION NUMBER: US 60/54,758
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR FILING DATE: 2004-06-01
; PRIOR FILING DATE: 2004-11-30
PRIOR FILING DATE: 2004-04-23
PRIOR APPLICATION NUMBER: US 60/575,978
PRIOR PILING DATE: 2004-06-01
PRIOR PILING DATE: 2004-11-30
PRIOR PILING DATE: 2004-11-30
PRIOR APPLICATION NUMBER: US 60/633,826
PRIOR PILING DATE: 2004-12-07
NUMBER OF SEQ ID NOS: 511
SOFTWARE: Patentin vergion 3.3
SEQ ID NO 643
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SOFWARE: Patentin version 3.3
SEQ ID NO 30
LENGTH: 158692
                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-64
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ORGANISM: Homo sapiens
US-11-121-086-30
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US-11-121-086-30
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APPLICANT: NIELSEN, KIRSTEN V.
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
FILE REFERENCE: 09138.6000-00000
CURRENT APPLICATION NUMBER: US/11/12,086
CURRENT APPLICATION NUMBER: US/11/12,086
PRIOR APPLICATION NUMBER: 00/567,570
PRIOR APPLICATION NUMBER: 00/567,570
PRIOR FILING DATE: 2004-05-04
NUMBER OF SEQ ID NOS: 107
SOFTWARE: Patentin version 3.3
SEQ ID NO 36
LENGTH: 172649
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100.0%; Pred. No. 0.62;
tive 0; Mismatches 0; Indels 0;
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Pred. No. 0.62;
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APPLICANT: Davis, Lisa M.
TITLE OF INVENTION: Breast Cancer Biomarkers
FILE OF INVENTION: Breast Cancer Biomarkers
FILE OF INVENTION: UNBER: US/11/112,908
CURRENT APPLICATION NUMBER: US 60/564,758
PRIOR FILING DATE: 2004-04-23
PRIOR FILING DATE: 2004-06-01
PRIOR FILING DATE: 2004-06-01
PRIOR FILING DATE: 2004-10-30
PRIOR FILING DATE: 2004-11-30
PRIOR FILING DATE: 2004-11-30
PRIOR PLILING DATE: 2004-11-30
PRIOR PLILING DATE: 2004-11-30
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; Publication No. US20050266459A1
; GENERAL INFORMATION:
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SOFTWARE: PatentIn version 3.3 SEQ ID NO 62 LENGTH: 170508
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SOFTWARE: PatentIn version 3.3
                                                                                                                                                                                                           Best Local Similarity 100.
Matches 24; Conservative
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US-11-121-086-36
                                                                                                    ; ORGANISM: Homo sapiens
US-11-112-908-62
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Query Match 1.3%; Score 24; DB 7; Length 173115; Best Local Similarity 100.0%; Pred. No. 0.62; Matches 24; Conservative 0; Mismatches 0; Indels 0.
                                                                                                                                                                                                          RESULT 15

US-11-112-908-32

Sequence 32, Application US/11112908

Publication No. US20050260659A1

GENERAL INFORMATION:

APPLICANT: Harris, Cole

APPLICANT: Barsis, Cole

TITLE OF INVENTION: Breast Cancer Biomarkers

FILE REFERENCE: 04-164-US

CURRENT FILING DATE: 2005-04-22

PRIOR FILING DATE: 2006-04-22

PRIOR APPLICATION NUMBER: US/11/112,908

CURRENT FILING DATE: 2004-04-23

PRIOR APPLICATION NUMBER: US 60/554,758

PRIOR APPLICATION NUMBER: US 60/631,702

PRIOR APPLICATION NUMBER: US 60/631,702

PRIOR FILING DATE: 2004-11-30

PRIOR FILING DATE: 2004-11-30

NUMBER OF SEQ ID NOS: 511

SOFTWARE: Patentin version 3.3

LENGTH: 193363

TTYPE: DNA

ORGANISM: Homo sapiens

US-11-112-908-32
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Search completed: December 30, 2005, 09:39:32 Job time : 302 secs

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1816 ACTGTAAAAAAAAAAAAAAAA 1839

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